

SCORE Search Results Details for Application 10667096
and Search Result us-10-667-096-34.rag.

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This page gives you Search Results detail for the Application 10667096 and Search Result us-10-667-096-34.rag.
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 25, 2006, 09:36:50 ; Search time 83 Seconds
(without alignments)
82.629 Million cell updates/sec

Title: US-10-667-096-34
Perfect score: 62
Sequence: 1 IEGPTLRQXLAARAX 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	62	100.0	36	3	AA	96522	Aay96522 Linear th
2	62	100.0	36	3	AA	17300	Aab17300 TPO-mimet
3	62	100.0	36	10	AE	F62114	Aef62114 Modified
4	62	100.0	36	10	AE	F62130	Aef62130 Modified
5	61	98.4	14	8	AD	M72475	Adm72475 TPO mimet
6	61	98.4	14	9	AD	Y64334	Ady64334 Thrombopo
7	61	98.4	15	8	AD	M72477	Adm72477 TPO mimet
8	61	98.4	15	9	AD	Y64335	Ady64335 Thrombopo
9	61	98.4	16	2	AA	W66711	Aaw66711 Peptide c
10	61	98.4	16	8	AD	M72476	Adm72476 TPO mimet
11	60	96.8	14	2	AA	W09463	Aaw09463 Thrombopo
12	60	96.8	14	2	AA	W09468	Aaw09468 Thrombopo
13	60	96.8	14	2	AA	W33030	Aaw33030 Thrombopo
14	60	96.8	14	2	AA	W33034	Aaw33034 Thrombopo
15	60	96.8	14	2	AA	W36774	Aaw36774 Thrombopo
16	60	96.8	14	2	AD	I24843	Adi24843 AF 12505

17	60	96.8	14	3	AAy96515	Aay96515	Thrombopo
18	60	96.8	14	3	AAB16962	Aab16962	TPO-mimet
19	60	96.8	14	4	AAU25827	Aau25827	Human thr
20	60	96.8	14	4	AAU26004	Aau26004	Human thr
21	60	96.8	14	5	ABB72853	Abb72853	TPO mimet
22	60	96.8	14	5	ABP51669	Abp51669	Thrombopo
23	60	96.8	14	5	AAE18011	Aae18011	Human lig
24	60	96.8	14	6	ABG71747	Abg71747	TPO recep
25	60	96.8	14	7	ABR62907	Abr62907	Thrombopo
26	60	96.8	14	7	ADC33697	Adc33697	Erythropro
27	60	96.8	14	7	ADN59652	Adn59652	Thrombopo
28	60	96.8	14	8	ADL27293	Adl27293	Amino aci
29	60	96.8	14	8	ADM72483	Adm72483	TPO mimet
30	60	96.8	14	8	ADQ16584	Adq16584	Agonist T
31	60	96.8	14	8	ADT92482	Adt92482	Thrombopo
32	60	96.8	14	9	ADU70210	Adu70210	Thrombopo
33	60	96.8	14	9	ADU75982	Adu75982	Peptide-b
34	60	96.8	14	9	ADV44319	Adv44319	Agonist T
35	60	96.8	14	9	AEB12792	Aeb12792	TPO mimet
36	60	96.8	14	9	AEC75357	Aec75357	Amino aci
37	60	96.8	14	10	AEP61580	Aef61580	Modified
38	60	96.8	15	2	AAW35416	Aaw35416	Thrombopo
39	60	96.8	15	2	AAW36776	Aaw36776	Thrombopo
40	60	96.8	15	2	AAW66712	Aaw66712	Peptide c
41	60	96.8	15	3	AAB20684	Aab20684	Thrombocy
42	60	96.8	15	4	AAU25996	Aau25996	Human thr
43	60	96.8	15	4	AAU25831	Aau25831	Human thr
44	60	96.8	15	5	ABP51670	Abp51670	Thrombopo
45	60	96.8	15	7	ABR62908	Abr62908	Thrombopo
46	60	96.8	15	8	ADM72485	Adm72485	TPO mimet
47	60	96.8	15	8	ADM72479	Adm72479	TPO mimet
48	60	96.8	15	8	ADM72478	Adm72478	TPO mimet
49	60	96.8	15	8	ADM72533	Adm72533	TPO mimet
50	60	96.8	15	8	ADM72522	Adm72522	TPO mimet
51	60	96.8	15	8	ADM72523	Adm72523	TPO mimet
52	60	96.8	15	8	ADM72482	Adm72482	TPO mimet
53	60	96.8	15	8	ADQ16585	Adq16585	TPO mimet
54	60	96.8	15	8	ADT92483	Adt92483	Modified
55	60	96.8	15	9	ADU70209	Adu70209	Thrombopo
56	60	96.8	15	9	ADU75981	Adu75981	Peptide-b
57	60	96.8	15	9	ADV44320	Adv44320	Agonist T
58	60	96.8	15	9	AEB12793	Aeb12793	TPO mimet
59	60	96.8	16	2	AAW19534	Aaw19534	Thrombopo
60	60	96.8	16	2	AAW33035	Aaw33035	Thrombopo
61	60	96.8	16	2	AAW36775	Aaw36775	Thrombopo
62	60	96.8	16	2	AAW36771	Aaw36771	Thrombopo
63	60	96.8	16	2	AAW66709	Aaw66709	Peptide c
64	60	96.8	16	2	AAW66713	Aaw66713	Peptide c
65	60	96.8	16	2	AAW66733	Aaw66733	Peptide c
66	60	96.8	16	2	AAW66716	Aaw66716	Peptide c
67	60	96.8	16	4	AAU26005	Aau26005	Human thr
68	60	96.8	16	4	AAU26043	Aau26043	Human thr
69	60	96.8	16	4	AAU25832	Aau25832	Human thr
70	60	96.8	16	8	ADM72532	Adm72532	TPO mimet
71	60	96.8	16	8	ADM72484	Adm72484	TPO mimet
72	60	96.8	18	3	AAB16957	Aab16957	PEGylated
73	60	96.8	18	3	AAB16956	Aab16956	PEGylated
74	60	96.8	18	5	ABP51687	Abp51687	TPO mimet
75	60	96.8	18	5	ABP51689	Abp51689	TPO mimet
76	60	96.8	18	5	ABP51688	Abp51688	TPO mimet
77	60	96.8	18	5	ABP51677	Abp51677	TPO mimet
78	60	96.8	18	5	ABP51686	Abp51686	TPO mimet
79	60	96.8	18	5	ABP51674	Abp51674	TPO mimet
80	60	96.8	18	5	ABP51693	Abp51693	TPO mimet
81	60	96.8	18	5	ABP51684	Abp51684	TPO mimet
82	60	96.8	18	5	ABP51683	Abp51683	TPO mimet
83	60	96.8	18	5	ABP51685	Abp51685	TPO mimet
84	60	96.8	18	5	ABP51691	Abp51691	TPO mimet
85	60	96.8	18	5	ABP51673	Abp51673	TPO mimet
86	60	96.8	18	5	ABP51690	Abp51690	TPO mimet
87	60	96.8	18	5	ABP51675	Abp51675	TPO mimet
88	60	96.8	18	5	ABP51692	Abp51692	TPO mimet
89	60	96.8	18	7	ADN59812	Adn59812	Thrombopo
90	60	96.8	18	8	ADQ16611	Adq16611	TPO mimet
91	60	96.8	18	8	ADQ16619	Adq16619	TPO mimet
92	60	96.8	18	8	ADQ16621	Adq16621	TPO mimet
93	60	96.8	18	8	ADQ16641	Adq16641	TPO mimet
94	60	96.8	18	8	ADQ16646	Adq16646	TPO mimet
95	60	96.8	18	8	ADQ16607	Adq16607	TPO mimet
96	60	96.8	18	8	ADQ16615	Adq16615	TPO mimet
97	60	96.8	18	8	ADQ16627	Adq16627	TPO mimet

98	60	96.8	18	8	ADQ16625	Adq16625 TPO mimet
99	60	96.8	18	8	ADQ16617	Adq16617 TPO mimet
100	60	96.8	18	8	ADQ16629	Adq16629 TPO mimet
101	60	96.8	18	8	ADQ16613	Adq16613 TPO mimet
102	60	96.8	18	8	ADQ16623	Adq16623 TPO mimet
103	60	96.8	18	8	ADQ16605	Adq16605 TPO mimet
104	60	96.8	18	8	ADQ16609	Adq16609 TPO mimet
105	60	96.8	18	9	ADV44355	Adv44355 Agonist T
106	60	96.8	18	9	ADV44345	Adv44345 Agonist T
107	60	96.8	18	9	ADV44351	Adv44351 Agonist T
108	60	96.8	18	9	ADV44357	Adv44357 Agonist T
109	60	96.8	18	9	ADV44349	Adv44349 Agonist T
110	60	96.8	18	9	ADV44343	Adv44343 Agonist T
111	60	96.8	18	9	ADV44347	Adv44347 Agonist T
112	60	96.8	18	9	ADV44384	Adv44384 Agonist T
113	60	96.8	18	9	ADV44353	Adv44353 Agonist T
114	60	96.8	18	9	ADV44363	Adv44363 Agonist T
115	60	96.8	18	9	ADV44361	Adv44361 Agonist T
116	60	96.8	18	9	ADV44379	Adv44379 Agonist T
117	60	96.8	18	9	ADV44344	Adv44344 Agonist T
118	60	96.8	18	9	ADV44359	Adv44359 Agonist T
119	60	96.8	18	9	ADV44365	Adv44365 Agonist T
120	60	96.8	18	9	ADV44367	Adv44367 Agonist T
121	60	96.8	18	9	ADV44468	Adv44468 Agonist T
122	60	96.8	18	9	AEB12826	Aeb12826 TPO mimet
123	60	96.8	18	9	AEB12820	Aeb12820 TPO mimet
124	60	96.8	18	9	AEB12840	Aeb12840 TPO mimet
125	60	96.8	18	9	AEB12857	Aeb12857 Antibody
126	60	96.8	18	9	AEB12834	Aeb12834 TPO mimet
127	60	96.8	18	9	AEB12830	Aeb12830 TPO mimet
128	60	96.8	18	9	AEB12939	Aeb12939 TPO mimet
129	60	96.8	18	9	AEB12832	Aeb12832 TPO mimet
130	60	96.8	18	9	AEB12852	Aeb12852 TPO mimet
131	60	96.8	18	9	AEB12816	Aeb12816 TPO mimet
132	60	96.8	18	9	AEB12818	Aeb12818 TPO mimet
133	60	96.8	18	9	AEB12828	Aeb12828 TPO mimet
134	60	96.8	18	9	AEB12836	Aeb12836 TPO mimet
135	60	96.8	18	9	AEB12822	Aeb12822 TPO mimet
136	60	96.8	18	9	AEB12824	Aeb12824 TPO mimet
137	60	96.8	18	9	AEB12838	Aeb12838 TPO mimet
138	60	96.8	19	5	ABB73391	Abb73391 TPO-mimet
139	60	96.8	19	5	ABB73390	Abb73390 TPO-mimet
140	60	96.8	20	3	AAB18003	Aab18003 Fc-TMP pe
141	60	96.8	20	3	AAB17929	Aab17929 TPO-mimet
142	60	96.8	20	5	ABB73403	Abb73403 TPO mimet
143	60	96.8	20	9	AEC75371	Aec75371 Peptide 1
144	60	96.8	21	7	ADN59687	Adn59687 Thrombopo
145	60	96.8	22	7	ADN59819	Adn59819 TMP pepti
146	60	96.8	22	8	ADQ16714	Adq16714 Immunoglo
147	60	96.8	22	8	ADQ16713	Adq16713 Immunoglo
148	60	96.8	22	8	ADQ16709	Adq16709 Immunoglo
149	60	96.8	22	8	ADQ16706	Adq16706 Immunoglo
150	60	96.8	22	8	ADQ16699	Adq16699 TPO mimet
151	60	96.8	22	8	ADQ16712	Adq16712 Immunoglo
152	60	96.8	22	8	ADQ16707	Adq16707 Immunoglo
153	60	96.8	22	8	ADQ16711	Adq16711 Immunoglo
154	60	96.8	22	8	ADQ16708	Adq16708 Immunoglo
155	60	96.8	22	8	ADQ16710	Adq16710 Immunoglo
156	60	96.8	22	9	ADV44435	Adv44435 Modified
157	60	96.8	22	9	ADV44449	Adv44449 Anti-teta
158	60	96.8	22	9	ADV44443	Adv44443 Anti-teta
159	60	96.8	22	9	ADV44444	Adv44444 Anti-teta
160	60	96.8	22	9	ADV44448	Adv44448 Anti-teta
161	60	96.8	22	9	ADV44442	Adv44442 Anti-teta
162	60	96.8	22	9	ADV44447	Adv44447 Anti-teta
163	60	96.8	22	9	ADV44445	Adv44445 Anti-teta
164	60	96.8	22	9	ADV44450	Adv44450 Anti-teta
165	60	96.8	22	9	ADV44446	Adv44446 Anti-teta
166	60	96.8	22	9	AEB12918	Aeb12918 TPO mimet
167	60	96.8	22	9	AEB12917	Aeb12917 TPO mimet
168	60	96.8	22	9	AEB12919	Aeb12919 TPO mimet
169	60	96.8	22	9	AEB12986	Aeb12986 TT antibo
170	60	96.8	22	9	AEB12920	Aeb12920 TPO mimet
171	60	96.8	22	9	AEB12916	Aeb12916 TPO mimet
172	60	96.8	22	9	AEB12914	Aeb12914 TPO mimet
173	60	96.8	22	9	AEB12921	Aeb12921 TPO mimet
174	60	96.8	22	9	AEB12907	Aeb12907 TT antibo
175	60	96.8	22	9	AEB12915	Aeb12915 TPO mimet
176	60	96.8	28	3	AAB17285	Aab17285 TPO-mimet
177	60	96.8	28	5	ABP51682	Abp51682 TPO mimet
178	60	96.8	28	7	ADJ73013	Adj73013 TPO mimet

179	60	96.8	28	8	ADJ52648	Adj52648 CH1 delet
180	60	96.8	28	8	ADJ52647	Adj52647 CH1 delet
181	60	96.8	28	8	ADJ51609	Adj51609 CH1 delet
182	60	96.8	28	8	ADQ16636	Adq16636 Tetanus t
183	60	96.8	28	9	ADV44374	Adv44374 Modified
184	60	96.8	28	9	AEB12847	Aeb12847 Antibody
185	60	96.8	28	10	AEF61583	Aef61583 Modified
186	60	96.8	29	3	AAB16975	Aab16975 TPO-mimet
187	60	96.8	29	3	AAB16976	Aab16976 TPO-mimet
188	60	96.8	29	3	AAB17286	Aab17286 TPO-mimet
189	60	96.8	29	3	AAB16970	Aab16970 TPO-mimet
190	60	96.8	29	3	AAB16972	Aab16972 TPO-mimet
191	60	96.8	29	5	ABB72862	Abb72862 TPO mimet
192	60	96.8	29	5	ABB72861	Abb72861 TPO mimet
193	60	96.8	29	5	ABB72858	Abb72858 TPO mimet
194	60	96.8	29	5	ABB72856	Abb72856 TPO mimet
195	60	96.8	29	7	ADJ73011	Adj73011 TPO mimet
196	60	96.8	29	7	ADJ73012	Adj73012 TPO mimet
197	60	96.8	29	7	ADJ73006	Adj73006 TPO mimet
198	60	96.8	29	7	ADJ73008	Adj73008 TPO mimet
199	60	96.8	29	8	ADJ52646	Adj52646 CH1 delet
200	60	96.8	29	8	ADJ52641	Adj52641 CH1 delet
201	60	96.8	29	8	ADJ52643	Adj52643 CH1 delet
202	60	96.8	29	8	ADJ51604	Adj51604 CH1 delet
203	60	96.8	29	8	ADJ51608	Adj51608 CH1 delet
204	60	96.8	29	8	ADJ51602	Adj51602 CH1 delet
205	60	96.8	29	8	ADJ51607	Adj51607 CH1 delet
206	60	96.8	29	10	AEF61588	Aef61588 Modified
207	60	96.8	29	10	AEF61586	Aef61586 Modified
208	60	96.8	29	10	AEF61587	Aef61587 Modified
209	60	96.8	29	10	AEF61589	Aef61589 Modified
210	60	96.8	29	10	AEF61585	Aef61585 Modified
211	60	96.8	30	3	AAB17287	Aab17287 TPO-mimet
212	60	96.8	31	3	AAB17288	Aab17288 TPO-mimet
213	60	96.8	31	3	AAB16974	Aab16974 TPO-mimet
214	60	96.8	31	3	AAB16973	Aab16973 TPO-mimet
215	60	96.8	31	5	ABB72860	Abb72860 TPO mimet
216	60	96.8	31	5	ABB72859	Abb72859 TPO mimet
217	60	96.8	31	7	ADJ73009	Adj73009 TPO mimet
218	60	96.8	31	7	ADJ73010	Adj73010 TPO mimet
219	60	96.8	31	8	ADJ52644	Adj52644 CH1 delet
220	60	96.8	31	8	ADJ52645	Adj52645 CH1 delet
221	60	96.8	31	8	ADJ51606	Adj51606 CH1 delet
222	60	96.8	31	8	ADJ51605	Adj51605 CH1 delet
223	60	96.8	32	3	AAY96520	Aay96520 Thrombopo
224	60	96.8	32	3	AAB17289	Aab17289 TPO-mimet
225	60	96.8	32	3	AAB17297	Aab17297 TPO-mimet
226	60	96.8	32	10	AEF62124	Aef62124 Modified
227	60	96.8	32	10	AEF62111	Aef62111 Modified
228	60	96.8	32	10	AEF62123	Aef62123 Modified
229	60	96.8	33	3	AAB17290	Aab17290 TPO-mimet
230	60	96.8	34	3	AAY96527	Aay96527 Thrombopo
231	60	96.8	34	3	AAB17291	Aab17291 TPO-mimet
232	60	96.8	34	10	AEF62126	Aef62126 Modified
233	60	96.8	35	3	AAB17292	Aab17292 TPO-mimet
234	60	96.8	36	3	AAY96521	Aay96521 Cyclic or
235	60	96.8	36	3	AAY96525	Aay96525 Thrombopo
236	60	96.8	36	3	AAY96523	Aay96523 Thrombopo
237	60	96.8	36	3	AAY96524	Aay96524 Thrombopo
238	60	96.8	36	3	AAY96526	Aay96526 Thrombopo
239	60	96.8	36	3	AAB17307	Aab17307 TPO-mimet
240	60	96.8	36	3	AAB17298	Aab17298 TPO-mimet
241	60	96.8	36	3	AAB17293	Aab17293 TPO-mimet
242	60	96.8	36	3	AAB17303	Aab17303 TPO-mimet
243	60	96.8	36	3	AAB16963	Aab16963 TPO-mimet
244	60	96.8	36	3	AAB17301	Aab17301 TPO-mimet
245	60	96.8	36	3	AAB17299	Aab17299 TPO-mimet
246	60	96.8	36	3	AAB17306	Aab17306 TPO-mimet
247	60	96.8	36	5	ABB72403	Abb72403 TPO-mimet
248	60	96.8	36	10	AEF62127	Aef62127 Modified
249	60	96.8	36	10	AEF62120	Aef62120 Modified
250	60	96.8	36	10	AEF62128	Aef62128 Modified
251	60	96.8	36	10	AEF62132	Aef62132 Modified
252	60	96.8	36	10	AEF62122	Aef62122 Modified
253	60	96.8	36	10	AEF62117	Aef62117 Modified
254	60	96.8	36	10	AEF62133	Aef62133 Modified
255	60	96.8	36	10	AEF62116	Aef62116 Modified
256	60	96.8	36	10	AEF62119	Aef62119 Modified
257	60	96.8	36	10	AEF62121	Aef62121 Modified
258	60	96.8	36	10	AEF62125	Aef62125 Modified
259	60	96.8	36	10	AEF62131	Aef62131 Modified

260	60	96.8	36	10	AEF62113	Aef62113 Modified
261	60	96.8	36	10	AEF62134	Aef62134 Modified
262	60	96.8	36	10	AEF62115	Aef62115 Modified
263	60	96.8	36	10	AEF62129	Aef62129 Modified
264	60	96.8	36	10	AEF62112	Aef62112 Modified
265	60	96.8	36	10	AEF62118	Aef62118 Modified
266	60	96.8	37	3	AAB17294	Aab17294 TPO-mimet
267	60	96.8	38	3	AAB17295	Aab17295 TPO-mimet
268	60	96.8	39	3	AAB17304	Aab17304 TPO-mimet
269	60	96.8	39	3	AAB17305	Aab17305 TPO-mimet
270	60	96.8	40	3	AAB17302	Aab17302 TPO-mimet
271	60	96.8	41	3	AAY96528	Aay96528 Thrombopo
272	60	96.8	41	5	ABB73389	Abb73389 TPO-mimet
273	60	96.8	41	5	ABB73388	Abb73388 TPO-mimet
274	60	96.8	41	10	AEF61124	Aef61124 Modified
275	60	96.8	41	10	AEF62135	Aef62135 Modified
276	60	96.8	41	10	AEF61123	Aef61123 Modified
277	60	96.8	42	3	AAY96530	Aay96530 Thrombopo
278	60	96.8	42	3	AAB17296	Aab17296 TPO-mimet
279	60	96.8	42	3	AAB17308	Aab17308 Synthetic
280	60	96.8	42	3	AAB17282	Aab17282 TPO-mimet
281	60	96.8	42	3	AAB17281	Aab17281 TPO-mimet
282	60	96.8	42	5	ABB73404	Abb73404 TMP-TMP g
283	60	96.8	60	3	AAB17311	Aab17311 Synthetic
284	60	96.8	60	5	ABB73405	Abb73405 TMP-TMP g
285	60	96.8	122	9	ADV44474	Adv44474 Anti-teta
286	60	96.8	122	9	AEB12946	Aeb12946 Antibody
287	60	96.8	128	8	ADQ16705	Adq16705 Modified
288	60	96.8	128	9	ADV44466	Adv44466 Anti-teta
289	60	96.8	128	9	ADV44463	Adv44463 Anti-teta
290	60	96.8	128	9	ADV44467	Adv44467 Anti-teta
291	60	96.8	128	9	ADV44465	Adv44465 Anti-teta
292	60	96.8	128	9	ADV44441	Adv44441 pAX116 va
293	60	96.8	128	9	ADV44464	Adv44464 Anti-teta
294	60	96.8	128	9	AEB12934	Aeb12934 Antibody
295	60	96.8	128	9	AEB12935	Aeb12935 Antibody
296	60	96.8	128	9	AEB12913	Aeb12913 Antibody
297	60	96.8	128	9	AEB12936	Aeb12936 Antibody
298	60	96.8	128	9	AEB12937	Aeb12937 Antibody
299	60	96.8	128	9	AEB12938	Aeb12938 Antibody
300	60	96.8	129	6	ABG71751	Abg71751 Antibody
301	60	96.8	131	6	ABG71753	Abg71753 Antibody
302	60	96.8	132	9	ADV44473	Adv44473 Anti-teta
303	60	96.8	132	9	AEC75373	Aec75373 Peptide g
304	60	96.8	133	6	ABG71752	Abg71752 Antibody
305	60	96.8	133	9	AEC75379	Aec75379 Peptide g
306	60	96.8	134	9	AEC75394	Aec75394 Amino aci
307	60	96.8	135	6	ABG71749	Abg71749 Antibody
308	60	96.8	143	6	ABG71750	Abg71750 Antibody
309	60	96.8	144	6	ABG71748	Abg71748 Antibody
310	60	96.8	150	9	AEB12945	Aeb12945 Antibody
311	60	96.8	225	8	ADQ16704	Adq16704 Modified
312	60	96.8	234	9	AEB12912	Aeb12912 Antibody
313	60	96.8	247	3	AAB16958	Aab16958 Fc-TMP pr
314	60	96.8	247	3	AAB16961	Aab16961 TMP-Fc pr
315	60	96.8	247	5	ABB73411	Abb73411 Fc-TPO mi
316	60	96.8	247	5	ABB73414	Abb73414 TMP-Fc am
317	60	96.8	249	9	ADV44440	Adv44440 pAX116 va
318	60	96.8	266	10	AEF62145	Aef62145 Murine Fc
319	60	96.8	268	3	AAB16959	Aab16959 Fc-TMP-TM
320	60	96.8	268	5	ABB73412	Abb73412 Fc-TMP-TM
321	60	96.8	269	3	AAY96531	Aay96531 Human IgG
322	60	96.8	269	3	AAB16960	Aab16960 TMP-TMP-F
323	60	96.8	269	5	ABB73413	Abb73413 TMP-TMP-F
324	60	96.8	282	9	AEB12930	Aeb12930 Antibody
325	60	96.8	459	9	ADV44459	Adv44459 Anti-teta
326	60	96.8	472	5	ABP51695	Abp51695 5G1.1-TPO
327	60	96.8	472	8	ADQ16647	Adq16647 Immunoglo
328	60	96.8	472	9	ADV44385	Adv44385 5G1.1 hea
329	60	96.8	472	9	AEB12858	Aeb12858 Antibody
330	57	91.9	14	3	AAB16969	Aab16969 TPO-mimet
331	57	91.9	14	3	AAB16968	Aab16968 TPO-mimet
332	57	91.9	14	5	ABB72854	Abb72854 TPO mimet
333	57	91.9	14	5	ABB72855	Abb72855 TPO mimet
334	57	91.9	14	7	ADJ73005	Adj73005 TPO mimet
335	57	91.9	14	7	ADJ73004	Adj73004 TPO mimet
336	57	91.9	14	8	ADJ52639	Adj52639 CH1 delet
337	57	91.9	14	8	ADJ52640	Adj52640 CH1 delet
338	57	91.9	14	8	ADJ51601	Adj51601 CH1 delet
339	57	91.9	14	8	ADJ51600	Adj51600 CH1 delet
340	57	91.9	14	8	ADM72507	Adm72507 TPO mimet

341	57	91.9	14	8	ADM72505	Adm72505 TPO mimet
342	57	91.9	14	8	ADM72509	Adm72509 TPO mimet
343	57	91.9	14	8	ADM72501	Adm72501 TPO mimet
344	57	91.9	14	9	ADU70205	Adu70205 Thrombopo
345	57	91.9	14	9	ADU75978	Adu75978 Thrombopo
346	57	91.9	14	10	Aef61582	Aef61582 Modified
347	57	91.9	14	10	Aef61581	Aef61581 Modified
348	57	91.9	15	2	AAW66722	Aaw66722 Peptide c
349	57	91.9	15	2	AAW66720	Aaw66720 Peptide c
350	57	91.9	15	2	AAW66723	Aaw66723 Peptide c
351	57	91.9	15	2	AAW66718	Aaw66718 Peptide c
352	57	91.9	15	4	AAU25833	Aau25833 Human thr
353	57	91.9	15	4	AAU26027	Aau26027 Human thr
354	57	91.9	15	4	AAU26025	Aau26025 Human thr
355	57	91.9	15	4	AAU26028	Aau26028 Human thr
356	57	91.9	15	8	ADM72506	Adm72506 TPO mimet
357	57	91.9	15	8	ADM72500	Adm72500 TPO mimet
358	57	91.9	15	8	ADM72508	Adm72508 TPO mimet
359	57	91.9	15	8	ADM72504	Adm72504 TPO mimet
360	57	91.9	28	10	Aef61584	Aef61584 Modified
361	57	91.9	29	3	AAB16971	Aab16971 TPO-mimet
362	57	91.9	29	5	ABB72857	Abb72857 TPO mimet
363	57	91.9	29	7	ADJ73007	Adj73007 TPO mimet
364	57	91.9	29	8	ADJ52642	Adj52642 CH1 delet
365	57	91.9	29	8	ADJ51603	Adj51603 CH1 delet
366	57	91.9	30	9	ADY64336	Ady64336 Thrombopo
367	56	90.3	13	2	AAW36779	Aaw36779 Thrombopo
368	56	90.3	13	7	ADJ73003	Adj73003 TPO mimet
369	56	90.3	13	8	ADJ52638	Adj52638 CH1 delet
370	56	90.3	13	8	ADJ51599	Adj51599 CH1 delet
371	56	90.3	14	4	AAU26006	Aau26006 Human thr
372	56	90.3	14	4	AAU26010	Aau26010 Human thr
373	56	90.3	14	8	ADM72503	Adm72503 TPO mimet
374	56	90.3	14	8	ADM72487	Adm72487 TPO mimet
375	56	90.3	14	9	ADU70206	Adu70206 Thrombopo
376	56	90.3	14	9	ADU75979	Adu75979 Thrombopo
377	56	90.3	15	2	AAW36784	Aaw36784 Thrombopo
378	56	90.3	15	2	AAW36780	Aaw36780 Thrombopo
379	56	90.3	15	2	AAW66714	Aaw66714 Peptide c
380	56	90.3	15	2	AAW66721	Aaw66721 Peptide c
381	56	90.3	15	4	AAU26026	Aau26026 Human thr
382	56	90.3	15	4	AAU26011	Aau26011 Human thr
383	56	90.3	15	4	AAU26020	Aau26020 Human thr
384	56	90.3	15	4	AAU26007	Aau26007 Human thr
385	56	90.3	15	8	ADM72502	Adm72502 TPO mimet
386	56	90.3	15	8	ADM72492	Adm72492 TPO mimet
387	56	90.3	15	8	ADM72490	Adm72490 TPO mimet
388	56	90.3	15	8	ADM72486	Adm72486 TPO mimet
389	56	90.3	15	8	ADM72491	Adm72491 TPO mimet
390	56	90.3	15	8	ADM72493	Adm72493 TPO mimet
391	56	90.3	16	4	AAU26021	Aau26021 Human thr
392	54	87.1	14	8	ADM72495	Adm72495 TPO mimet
393	54	87.1	14	8	ADM72497	Adm72497 TPO mimet
394	54	87.1	15	2	AAW66719	Aaw66719 Peptide c
395	54	87.1	15	2	AAW66724	Aaw66724 Peptide c
396	54	87.1	15	4	AAU26022	Aau26022 Human thr
397	54	87.1	15	4	AAU26016	Aau26016 Human thr
398	54	87.1	15	4	AAU26023	Aau26023 Human thr
399	54	87.1	15	8	ADM72480	Adm72480 TPO mimet
400	54	87.1	15	8	ADM72481	Adm72481 TPO mimet
401	54	87.1	15	8	ADM72496	Adm72496 TPO mimet
402	54	87.1	15	8	ADM72494	Adm72494 TPO mimet
403	54	87.1	16	4	AAU26017	Aau26017 Human thr
404	53	85.5	13	4	AAU26008	Aau26008 Human thr
405	52	83.9	12	2	AAW36787	Aaw36787 Thrombopo
406	52	83.9	13	4	AAU26012	Aau26012 Human thr
407	52	83.9	14	2	AAW36788	Aaw36788 Thrombopo
408	52	83.9	14	4	AAU26013	Aau26013 Human thr
409	52	83.9	14	8	ADM72511	Adm72511 TPO mimet
410	52	83.9	14	8	ADM72519	Adm72519 TPO mimet
411	52	83.9	15	2	AAW66717	Aaw66717 Peptide c
412	52	83.9	15	2	AAW66728	Aaw66728 Peptide c
413	52	83.9	15	4	AAU26033	Aau26033 Human thr
414	52	83.9	15	4	AAU26029	Aau26029 Human thr
415	52	83.9	15	8	ADM72510	Adm72510 TPO mimet
416	52	83.9	15	8	ADM72518	Adm72518 TPO mimet
417	51	82.3	12	2	AAW36781	Aaw36781 Thrombopo
418	51	82.3	14	2	AAW36782	Aaw36782 Thrombopo
419	51	82.3	14	4	AAU26009	Aau26009 Human thr
420	51	82.3	15	2	AAW66725	Aaw66725 Peptide c
421	51	82.3	18	7	ADN59663	Adn59663 Thrombopo

422	51	82.3	22	7	ADN59830	Adn59830	TMP	pepti
423	51	82.3	25	7	ADN59708	Adn59708	Thrombopo	
424	51	82.3	43	7	ADN59759	Adn59759	Peptide-v	
425	49	79.0	12	4	AAU26014	Aau26014	Human thr	
426	49	79.0	14	8	ADM72513	Adm72513	TPO mimet	
427	49	79.0	15	4	AAU25834	Aau25834	Human thr	
428	49	79.0	15	4	AAU26030	Aau26030	Human thr	
429	49	79.0	15	8	ADM72512	Adm72512	TPO mimet	
430	48	77.4	14	4	AAU26037	Aau26037	Human thr	
431	48	77.4	14	8	ADM72526	Adm72526	TPO mimet	
432	48	77.4	14	8	ADM72499	Adm72499	TPO mimet	
433	48	77.4	14	8	ADM72527	Adm72527	TPO mimet	
434	48	77.4	15	2	AAW66726	Aaw66726	Peptide c	
435	48	77.4	15	2	AAW66731	Aaw66731	Peptide c	
436	48	77.4	15	4	AAU26024	Aau26024	Human thr	
437	48	77.4	15	4	AAU26038	Aau26038	Human thr	
438	48	77.4	15	8	ADM72498	Adm72498	TPO mimet	
439	47	75.8	13	2	AAW36792	Aaw36792	Thrombopo	
440	47	75.8	13	4	AAU26015	Aau26015	Human thr	
441	47	75.8	19	2	AAW09491	Aaw09491	Thrombopo	
442	47	75.8	19	2	AAW09493	Aaw09493	Thrombopo	
443	47	75.8	19	2	AAW36644	Aaw36644	Thrombopo	
444	47	75.8	19	2	AAW35418	Aaw35418	Thrombopo	
445	47	75.8	19	2	AAW36642	Aaw36642	Thrombopo	
446	47	75.8	19	4	AAU25861	Aau25861	Human thr	
447	47	75.8	19	4	AAU25863	Aau25863	Human thr	
448	47	75.8	19	4	AAU25998	Aau25998	Human thr	
449	46	74.2	14	8	ADM72515	Adm72515	TPO mimet	
450	46	74.2	14	8	ADM72521	Adm72521	TPO mimet	
451	46	74.2	15	2	AAW66729	Aaw66729	Peptide c	
452	46	74.2	15	4	AAU26031	Aau26031	Human thr	
453	46	74.2	15	4	AAU26034	Aau26034	Human thr	
454	46	74.2	15	8	ADM72520	Adm72520	TPO mimet	
455	46	74.2	15	8	ADM72514	Adm72514	TPO mimet	
456	46	74.2	18	2	AAW09460	Aaw09460	Thrombopo	
457	46	74.2	18	2	AAW09498	Aaw09498	Thrombopo	
458	46	74.2	18	2	AAW36649	Aaw36649	Thrombopo	
459	46	74.2	18	2	AAW33027	Aaw33027	Thrombopo	
460	46	74.2	18	2	AAW36652	Aaw36652	Thrombopo	
461	46	74.2	18	3	AAB17026	Aab17026	TPO-mimet	
462	46	74.2	18	4	AAU25868	Aau25868	Human thr	
463	46	74.2	18	4	AAU25824	Aau25824	Human thr	
464	46	74.2	18	4	AAU25871	Aau25871	Human thr	
465	46	74.2	18	5	ABB72912	Abb72912	TPO mimet	
466	46	74.2	18	7	ADJ73064	Adj73064	TPO mimet	
467	46	74.2	18	8	ADJ52699	Adj52699	CH1 delet	
468	46	74.2	18	8	ADJ51660	Adj51660	CH1 delet	
469	46	74.2	18	10	AEF61632	Aef61632	Modified	
470	45	72.6	13	2	AAW36783	Aaw36783	Thrombopo	
471	45	72.6	13	4	AAU26035	Aau26035	Human thr	
472	45	72.6	13	8	ADM72524	Adm72524	TPO mimet	
473	45	72.6	14	2	AAW36773	Aaw36773	Thrombopo	
474	45	72.6	15	2	AAW66727	Aaw66727	Peptide c	
475	44	71.0	13	4	AAU26018	Aau26018	Human thr	
476	44	71.0	13	8	ADM72488	Adm72488	TPO mimet	
477	44	71.0	18	2	AAW09499	Aaw09499	Thrombopo	
478	44	71.0	18	2	AAW09459	Aaw09459	Thrombopo	
479	44	71.0	18	2	AAW36650	Aaw36650	Thrombopo	
480	44	71.0	18	2	AAW33026	Aaw33026	Thrombopo	
481	44	71.0	18	3	AAB17024	Aab17024	TPO-mimet	
482	44	71.0	18	4	AAU25869	Aau25869	Human thr	
483	44	71.0	18	4	AAU25823	Aau25823	Human thr	
484	44	71.0	18	5	ABB72910	Abb72910	TPO mimet	
485	44	71.0	18	7	ADJ73062	Adj73062	TPO mimet	
486	44	71.0	18	8	ADJ52697	Adj52697	CH1 delet	
487	44	71.0	18	8	ADJ51658	Adj51658	CH1 delet	
488	44	71.0	18	10	AEF61630	Aef61630	Modified	
489	43	69.4	10	3	AAB17006	Aab17006	TPO-mimet	
490	43	69.4	10	5	ABB72892	Abb72892	TPO mimet	
491	43	69.4	10	7	ADJ73043	Adj73043	TPO mimet	
492	43	69.4	10	8	ADJ52678	Adj52678	CH1 delet	
493	43	69.4	10	8	ADJ51639	Adj51639	CH1 delet	
494	43	69.4	10	10	AEF61615	Aef61615	Modified	
495	43	69.4	13	8	ADM72525	Adm72525	TPO mimet	
496	43	69.4	13	8	ADM72489	Adm72489	TPO mimet	
497	43	69.4	14	2	AAW66715	Aaw66715	Peptide c	
498	43	69.4	14	2	AAW66730	Aaw66730	Peptide c	
499	43	69.4	14	4	AAU26019	Aau26019	Human thr	
500	43	69.4	14	4	AAU26036	Aau26036	Human thr	
501	43	69.4	14	8	ADM72517	Adm72517	TPO mimet	
502	43	69.4	15	4	AAU26032	Aau26032	Human thr	

SCORE Search Results Details for Application 10667096 and Search Result us-10-667-096-34.rai.

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OM protein - protein search, using sw model

Run on: July 25, 2006, 09:44:29 ; Search time 51 Seconds
(without alignments)
25.744 Million cell updates/sec

Title: US-10-667-096-34
Perfect score: 62
Sequence: 1 IEGPTLRQXLAARAX 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	62	100.0	36	2	US-09-422-838C-13	Sequence 13, Appl
2	62	100.0	36	2	US-09-422-838C-29	Sequence 29, Appl
3	60	96.8	14	1	US-08-764-640-13	Sequence 13, Appl
4	60	96.8	14	1	US-08-764-640-193	Sequence 193, App
5	60	96.8	14	2	US-08-973-225-13	Sequence 13, Appl
6	60	96.8	14	2	US-08-973-225-193	Sequence 193, App
7	60	96.8	14	2	US-09-244-298A-13	Sequence 13, Appl
8	60	96.8	14	2	US-09-244-298A-193	Sequence 193, App
9	60	96.8	14	2	US-09-516-704-13	Sequence 13, Appl
10	60	96.8	14	2	US-09-516-704-193	Sequence 193, App
11	60	96.8	14	2	US-09-549-090-13	Sequence 13, Appl
12	60	96.8	14	2	US-09-549-090-193	Sequence 193, App
13	60	96.8	14	2	US-09-832-230A-13	Sequence 13, Appl
14	60	96.8	14	2	US-09-832-230A-193	Sequence 193, App
15	60	96.8	14	2	US-09-428-082B-13	Sequence 13, Appl
16	60	96.8	14	2	US-09-428-082B-26	Sequence 26, Appl
17	60	96.8	14	2	US-09-428-082B-28	Sequence 28, Appl
18	60	96.8	14	2	US-09-428-082B-29	Sequence 29, Appl
19	60	96.8	14	2	US-09-428-082B-30	Sequence 30, Appl

20	60	96.8	14	2	US-09-428-082B-31	Sequence 31, Appl
21	60	96.8	14	2	US-09-428-082B-32	Sequence 32, Appl
22	60	96.8	14	2	US-09-422-838C-1	Sequence 1, Appli
23	60	96.8	14	2	US-09-422-838C-2	Sequence 2, Appli
24	60	96.8	15	1	US-08-764-640-17	Sequence 17, Appl
25	60	96.8	15	1	US-08-764-640-185	Sequence 185, App
26	60	96.8	15	2	US-08-973-225-17	Sequence 17, Appl
27	60	96.8	15	2	US-08-973-225-185	Sequence 185, App
28	60	96.8	15	2	US-09-244-298A-17	Sequence 17, Appl
29	60	96.8	15	2	US-09-244-298A-185	Sequence 185, App
30	60	96.8	15	2	US-09-516-704-17	Sequence 17, Appl
31	60	96.8	15	2	US-09-516-704-185	Sequence 185, App
32	60	96.8	15	2	US-09-549-090-17	Sequence 17, Appl
33	60	96.8	15	2	US-09-549-090-185	Sequence 185, App
34	60	96.8	15	2	US-09-832-230A-17	Sequence 17, Appl
35	60	96.8	15	2	US-09-832-230A-185	Sequence 185, App
36	60	96.8	16	1	US-08-764-640-18	Sequence 18, Appl
37	60	96.8	16	1	US-08-764-640-194	Sequence 194, App
38	60	96.8	16	1	US-08-764-640-232	Sequence 232, App
39	60	96.8	16	2	US-08-973-225-18	Sequence 18, Appl
40	60	96.8	16	2	US-08-973-225-194	Sequence 194, App
41	60	96.8	16	2	US-08-973-225-220	Sequence 220, App
42	60	96.8	16	2	US-09-244-298A-18	Sequence 18, Appl
43	60	96.8	16	2	US-09-244-298A-194	Sequence 194, App
44	60	96.8	16	2	US-09-244-298A-232	Sequence 232, App
45	60	96.8	16	2	US-09-516-704-18	Sequence 18, Appl
46	60	96.8	16	2	US-09-516-704-194	Sequence 194, App
47	60	96.8	16	2	US-09-516-704-232	Sequence 232, App
48	60	96.8	16	2	US-09-549-090-18	Sequence 18, Appl
49	60	96.8	16	2	US-09-549-090-194	Sequence 194, App
50	60	96.8	16	2	US-09-549-090-220	Sequence 220, App
51	60	96.8	16	2	US-09-832-230A-18	Sequence 18, Appl
52	60	96.8	16	2	US-09-832-230A-194	Sequence 194, App
53	60	96.8	16	2	US-09-832-230A-232	Sequence 232, App
54	60	96.8	19	2	US-09-428-082B-1032	Sequence 1032, Ap
55	60	96.8	19	2	US-09-428-082B-1033	Sequence 1033, Ap
56	60	96.8	20	2	US-09-428-082B-368	Sequence 368, App
57	60	96.8	28	2	US-09-428-082B-341	Sequence 341, App
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Title: US-10-667-096-34
Perfect score: 62
Sequence: 1 IEGPTLRQXLAARAX 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

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Maximum DB seq length: 2000000000

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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57	60	96.8	14	5	US-10-645-784-28	Sequence 28, Appl
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63	60	96.8	14	6	US-11-254-419-193	Sequence 193, App
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69	60	96.8	15	4	US-10-307-724-2	Sequence 2, Appli
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72	60	96.8	15	5	US-10-645-784-30	Sequence 30, Appl
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Title: US-10-667-096-34
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

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SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	60	96.8	14	6	US-10-953-613C-462 Sequence 462, App
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10	60	96.8	269	7	US-11-234-731-617 Sequence 617, App
11	57	91.9	14	6	US-10-953-613C-458 Sequence 458, App
12	57	91.9	14	6	US-10-953-613C-459 Sequence 459, App
13	57	91.9	14	6	US-10-953-613C-461 Sequence 461, App
14	57	91.9	14	7	US-11-234-731-29 Sequence 29, Appl
15	57	91.9	14	7	US-11-234-731-30 Sequence 30, Appl
16	56	90.3	13	6	US-10-953-613C-457 Sequence 457, App
17	51	82.3	18	7	US-11-234-731-80 Sequence 80, Appl
18	46	74.2	18	6	US-10-953-613C-518 Sequence 518, App

19	46	74.2	18	7	US-11-234-731-69	Sequence 69, Appl
20	44	71.0	18	6	US-10-953-613C-516	Sequence 516, App
21	44	71.0	18	7	US-11-234-731-67	Sequence 67, Appl
22	43	69.4	10	6	US-10-953-613C-497	Sequence 497, App
23	43	69.4	10	7	US-11-234-731-53	Sequence 53, Appl
24	43	69.4	18	7	US-11-234-731-77	Sequence 77, Appl
25	43	69.4	18	7	US-11-234-731-81	Sequence 81, Appl
26	43	69.4	19	6	US-10-953-613C-514	Sequence 514, App
27	43	69.4	19	7	US-11-234-731-65	Sequence 65, Appl
28	41	66.1	18	7	US-11-234-731-83	Sequence 83, Appl
29	41	66.1	18	7	US-11-234-731-85	Sequence 85, Appl
30	40	64.5	18	7	US-11-234-731-92	Sequence 92, Appl
31	40	64.5	18	7	US-11-234-731-97	Sequence 97, Appl
32	40	64.5	18	7	US-11-234-731-98	Sequence 98, Appl
33	40	64.5	19	6	US-10-953-613C-513	Sequence 513, App
34	40	64.5	19	7	US-11-234-731-64	Sequence 64, Appl
35	40	64.5	254	7	US-11-234-731-654	Sequence 654, App
36	39	62.9	18	7	US-11-234-731-70	Sequence 70, Appl
37	39	62.9	18	7	US-11-234-731-84	Sequence 84, Appl
38	39	62.9	18	7	US-11-234-731-87	Sequence 87, Appl
39	38	61.3	18	7	US-11-234-731-71	Sequence 71, Appl
40	38	61.3	18	7	US-11-234-731-86	Sequence 86, Appl
41	38	61.3	18	7	US-11-234-731-95	Sequence 95, Appl
42	37	59.7	10	6	US-10-953-613C-496	Sequence 496, App
43	37	59.7	10	7	US-11-234-731-52	Sequence 52, Appl
44	37	59.7	18	7	US-11-234-731-74	Sequence 74, Appl
45	37	59.7	237	7	US-11-056-355B-27232	Sequence 27232, A
46	37	59.7	238	7	US-11-056-355B-27231	Sequence 27231, A
47	37	59.7	249	7	US-11-056-355B-27230	Sequence 27230, A
48	36	58.1	13	6	US-10-953-613C-506	Sequence 506, App
49	36	58.1	13	6	US-10-953-613C-510	Sequence 510, App
50	36	58.1	14	6	US-10-953-613C-507	Sequence 507, App
51	36	58.1	14	6	US-10-953-613C-508	Sequence 508, App
52	36	58.1	15	6	US-10-953-613C-509	Sequence 509, App
53	36	58.1	18	7	US-11-234-731-76	Sequence 76, Appl
54	36	58.1	18	7	US-11-234-731-88	Sequence 88, Appl
55	36	58.1	18	7	US-11-234-731-89	Sequence 89, Appl
56	36	58.1	254	7	US-11-234-731-653	Sequence 653, App
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58	35	56.5	18	7	US-11-234-731-78	Sequence 78, Appl
59	35	56.5	18	7	US-11-234-731-90	Sequence 90, Appl
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61	35	56.5	311	6	US-10-449-902-29837	Sequence 29837, A
62	35	56.5	311	6	US-10-449-902-46736	Sequence 46736, A
63	35	56.5	551	6	US-10-449-902-37558	Sequence 37558, A
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66	34	54.8	130	7	US-11-056-355B-60997	Sequence 60997, A
67	34	54.8	145	7	US-11-056-355B-52773	Sequence 52773, A
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69	34	54.8	236	7	US-11-056-355B-52771	Sequence 52771, A
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72	34	54.8	258	7	US-11-056-355B-35164	Sequence 35164, A
73	34	54.8	562	7	US-11-056-355B-7605	Sequence 7605, Ap
74	34	54.8	564	7	US-11-056-355B-7604	Sequence 7604, Ap
75	33	53.2	18	7	US-11-234-731-73	Sequence 73, Appl
76	33	53.2	18	7	US-11-234-731-75	Sequence 75, Appl
77	33	53.2	282	7	US-11-056-355B-17857	Sequence 17857, A
78	33	53.2	654	6	US-10-449-902-52096	Sequence 52096, A
79	33	53.2	664	6	US-10-471-571A-958	Sequence 958, App
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81	33	53.2	1118	6	US-10-506-630A-40	Sequence 40, Appl
82	32.5	52.4	512	7	US-11-174-307B-3790	Sequence 3790, Ap
83	32	51.6	14	6	US-10-953-613C-505	Sequence 505, App
84	32	51.6	14	7	US-11-234-731-61	Sequence 61, Appl
85	32	51.6	18	6	US-10-953-613C-512	Sequence 512, App
86	32	51.6	18	7	US-11-234-731-63	Sequence 63, Appl
87	32	51.6	143	7	US-11-056-355B-5763	Sequence 5763, Ap
88	32	51.6	204	7	US-11-056-355B-5762	Sequence 5762, Ap
89	32	51.6	237	6	US-10-953-349-27001	Sequence 27001, A
90	32	51.6	237	7	US-11-056-355B-68741	Sequence 68741, A
91	32	51.6	281	7	US-11-056-355B-5761	Sequence 5761, Ap
92	32	51.6	282	6	US-10-449-902-28479	Sequence 28479, A
93	32	51.6	282	6	US-10-449-902-49723	Sequence 49723, A
94	32	51.6	376	7	US-11-056-355B-16940	Sequence 16940, A
95	32	51.6	442	7	US-11-056-355B-16939	Sequence 16939, A
96	32	51.6	449	7	US-11-056-355B-16938	Sequence 16938, A
97	32	51.6	492	6	US-10-524-827-26	Sequence 26, Appl
98	32	51.6	535	7	US-11-056-355B-5444	Sequence 5444, Ap
99	32	51.6	766	6	US-10-449-902-42258	Sequence 42258, A

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103	31.5	50.8	307	6	US-10-953-349-29069	Sequence 29069, A
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106	31.5	50.8	332	7	US-11-056-355B-62746	Sequence 62746, A
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114	31	50.0	264	6	US-10-505-928-767	Sequence 767, App
115	31	50.0	287	7	US-11-293-697-2606	Sequence 2606, Ap
116	31	50.0	307	7	US-11-056-355B-15861	Sequence 15861, A
117	31	50.0	320	7	US-11-056-355B-11222	Sequence 11222, A
118	31	50.0	324	7	US-11-056-355B-15860	Sequence 15860, A
119	31	50.0	328	7	US-11-056-355B-47204	Sequence 47204, A
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121	31	50.0	336	7	US-11-056-355B-15859	Sequence 15859, A
122	31	50.0	356	7	US-11-056-355B-47203	Sequence 47203, A
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124	31	50.0	385	6	US-10-526-722-26	Sequence 26, Appl
125	31	50.0	385	6	US-10-526-722-68	Sequence 68, Appl
126	31	50.0	385	6	US-10-526-722-126	Sequence 126, App
127	31	50.0	484	7	US-11-056-355B-14293	Sequence 14293, A
128	31	50.0	500	6	US-10-449-902-38365	Sequence 38365, A
129	31	50.0	519	7	US-11-293-697-3767	Sequence 3767, Ap
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131	31	50.0	571	7	US-11-056-355B-14292	Sequence 14292, A
132	31	50.0	573	7	US-11-056-355B-47346	Sequence 47346, A
133	31	50.0	581	7	US-11-056-355B-47345	Sequence 47345, A
134	31	50.0	584	7	US-11-056-355B-47344	Sequence 47344, A
135	31	50.0	1132	6	US-10-526-722-42	Sequence 42, Appl
136	31	50.0	1162	6	US-10-449-902-44303	Sequence 44303, A
137	31	50.0	1162	6	US-10-449-902-56648	Sequence 56648, A
138	31	50.0	1500	6	US-10-526-722-100	Sequence 100, App
139	31	50.0	1589	6	US-10-526-722-158	Sequence 158, App
140	31	50.0	1822	6	US-10-505-928-700	Sequence 700, App
141	30	48.4	18	7	US-11-234-731-94	Sequence 94, Appl
142	30	48.4	18	7	US-11-234-731-96	Sequence 96, Appl
143	30	48.4	22	7	US-11-259-950-28	Sequence 28, Appl
144	30	48.4	83	7	US-11-056-355B-3613	Sequence 3613, Ap
145	30	48.4	84	7	US-11-056-355B-11145	Sequence 11145, A
146	30	48.4	94	6	US-10-449-902-34237	Sequence 34237, A
147	30	48.4	95	6	US-10-449-902-34803	Sequence 34803, A
148	30	48.4	117	6	US-10-471-571A-4784	Sequence 4784, Ap
149	30	48.4	168	7	US-11-259-950-12	Sequence 12, Appl
150	30	48.4	171	6	US-10-449-902-50689	Sequence 50689, A
151	30	48.4	179	7	US-11-259-950-63	Sequence 63, Appl
152	30	48.4	184	6	US-10-953-349-4034	Sequence 4034, Ap
153	30	48.4	189	7	US-11-259-950-56	Sequence 56, Appl
154	30	48.4	190	7	US-11-259-950-58	Sequence 58, Appl
155	30	48.4	190	7	US-11-259-950-60	Sequence 60, Appl
156	30	48.4	190	7	US-11-259-950-62	Sequence 62, Appl
157	30	48.4	199	7	US-11-259-950-67	Sequence 67, Appl
158	30	48.4	200	7	US-11-259-950-54	Sequence 54, Appl
159	30	48.4	201	7	US-11-259-950-6	Sequence 6, Appli
160	30	48.4	201	7	US-11-259-950-16	Sequence 16, Appl
161	30	48.4	201	7	US-11-259-950-17	Sequence 17, Appl
162	30	48.4	201	7	US-11-259-950-57	Sequence 57, Appl
163	30	48.4	201	7	US-11-259-950-59	Sequence 59, Appl
164	30	48.4	201	7	US-11-259-950-61	Sequence 61, Appl
165	30	48.4	208	6	US-10-953-349-4033	Sequence 4033, Ap
166	30	48.4	211	7	US-11-056-355B-37131	Sequence 37131, A
167	30	48.4	211	7	US-11-056-355B-101513	Sequence 101513,
168	30	48.4	211	7	US-11-056-355B-112752	Sequence 112752,
169	30	48.4	212	7	US-11-259-950-4	Sequence 4, Appli
170	30	48.4	212	7	US-11-259-950-55	Sequence 55, Appl
171	30	48.4	212	7	US-11-259-950-89	Sequence 89, Appl
172	30	48.4	212	7	US-11-259-950-91	Sequence 91, Appl
173	30	48.4	212	7	US-11-259-950-93	Sequence 93, Appl
174	30	48.4	215	7	US-11-056-355B-50214	Sequence 50214, A
175	30	48.4	216	7	US-11-056-355B-37130	Sequence 37130, A
176	30	48.4	216	7	US-11-056-355B-101512	Sequence 101512,
177	30	48.4	216	7	US-11-056-355B-112751	Sequence 112751,
178	30	48.4	223	7	US-11-259-950-53	Sequence 53, Appl
179	30	48.4	234	7	US-11-259-950-50	Sequence 50, Appl
180	30	48.4	243	6	US-10-538-916-3	Sequence 3, Appli

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183	30	48.4	256	7	US-11-259-950-51	Sequence 51, Appl
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185	30	48.4	278	6	US-10-449-902-31322	Sequence 31322, A
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187	30	48.4	278	7	US-11-259-950-65	Sequence 65, Appl
188	30	48.4	278	7	US-11-056-355B-37129	Sequence 37129, A
189	30	48.4	278	7	US-11-056-355B-101511	Sequence 101511,
190	30	48.4	278	7	US-11-056-355B-112750	Sequence 112750,
191	30	48.4	286	7	US-11-246-405-23	Sequence 23, Appl
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194	30	48.4	291	6	US-10-449-902-39294	Sequence 39294, A
195	30	48.4	333	6	US-10-953-349-15724	Sequence 15724, A
196	30	48.4	333	7	US-11-056-355B-53257	Sequence 53257, A
197	30	48.4	334	6	US-10-953-349-15723	Sequence 15723, A
198	30	48.4	334	7	US-11-056-355B-53256	Sequence 53256, A
199	30	48.4	335	7	US-11-056-355B-50213	Sequence 50213, A
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203	30	48.4	365	6	US-10-449-902-51634	Sequence 51634, A
204	30	48.4	366	6	US-10-953-349-36200	Sequence 36200, A
205	30	48.4	378	7	US-11-056-355B-47420	Sequence 47420, A
206	30	48.4	379	7	US-11-259-950-85	Sequence 85, Appl
207	30	48.4	381	7	US-11-259-950-70	Sequence 70, Appl
208	30	48.4	381	7	US-11-259-950-87	Sequence 87, Appl
209	30	48.4	383	7	US-11-259-950-83	Sequence 83, Appl
210	30	48.4	384	6	US-10-449-902-49110	Sequence 49110, A
211	30	48.4	392	7	US-11-259-950-18	Sequence 18, Appl
212	30	48.4	392	7	US-11-259-950-69	Sequence 69, Appl
213	30	48.4	397	7	US-11-259-950-81	Sequence 81, Appl
214	30	48.4	401	7	US-11-259-950-68	Sequence 68, Appl
215	30	48.4	407	6	US-10-449-902-35993	Sequence 35993, A
216	30	48.4	414	7	US-11-259-950-8	Sequence 8, Appli
217	30	48.4	418	6	US-10-953-349-24473	Sequence 24473, A
218	30	48.4	418	7	US-11-056-355B-57175	Sequence 57175, A
219	30	48.4	422	7	US-11-259-950-10	Sequence 10, Appl
220	30	48.4	423	7	US-11-259-950-66	Sequence 66, Appl
221	30	48.4	445	6	US-10-449-902-52501	Sequence 52501, A
222	30	48.4	457	7	US-11-056-355B-3192	Sequence 3192, Ap
223	30	48.4	459	6	US-10-449-902-46200	Sequence 46200, A
224	30	48.4	473	7	US-11-056-355B-45745	Sequence 45745, A
225	30	48.4	479	7	US-11-056-355B-47419	Sequence 47419, A
226	30	48.4	480	7	US-11-056-355B-3191	Sequence 3191, Ap
227	30	48.4	488	7	US-11-056-355B-47418	Sequence 47418, A
228	30	48.4	507	7	US-11-056-355B-3190	Sequence 3190, Ap
229	30	48.4	514	6	US-10-953-349-24472	Sequence 24472, A
230	30	48.4	514	7	US-11-056-355B-57174	Sequence 57174, A
231	30	48.4	531	7	US-11-056-355B-45744	Sequence 45744, A
232	30	48.4	547	7	US-11-174-307B-3732	Sequence 3732, Ap
233	30	48.4	562	6	US-10-449-902-42635	Sequence 42635, A
234	30	48.4	588	6	US-10-449-902-46341	Sequence 46341, A
235	30	48.4	615	6	US-10-449-902-34642	Sequence 34642, A
236	30	48.4	643	7	US-11-077-513-2	Sequence 2, Appli
237	30	48.4	709	6	US-10-828-564-15	Sequence 15, Appl
238	30	48.4	752	7	US-11-056-355B-69812	Sequence 69812, A
239	30	48.4	753	7	US-11-056-355B-88389	Sequence 88389, A
240	30	48.4	753	7	US-11-056-355B-92145	Sequence 92145, A
241	30	48.4	781	7	US-11-056-355B-69811	Sequence 69811, A
242	30	48.4	783	6	US-10-449-902-49312	Sequence 49312, A
243	30	48.4	1006	6	US-10-449-902-41503	Sequence 41503, A
244	30	48.4	1103	7	US-11-289-102-216	Sequence 216, App
245	30	48.4	1103	7	US-11-289-102-277	Sequence 277, App
246	30	48.4	1264	7	US-11-289-102-206	Sequence 206, App
247	30	48.4	1575	6	US-10-505-928-257	Sequence 257, App
248	29	46.8	16	7	US-11-340-003-20	Sequence 20, Appl
249	29	46.8	19	6	US-10-953-613C-515	Sequence 515, App
250	29	46.8	19	7	US-11-234-731-66	Sequence 66, Appl
251	29	46.8	76	6	US-10-449-902-39252	Sequence 39252, A
252	29	46.8	86	7	US-11-056-355B-51009	Sequence 51009, A
253	29	46.8	94	7	US-11-056-355B-37678	Sequence 37678, A
254	29	46.8	94	7	US-11-056-355B-77102	Sequence 77102, A
255	29	46.8	110	7	US-11-293-697-3777	Sequence 3777, Ap
256	29	46.8	110	7	US-11-056-355B-37677	Sequence 37677, A
257	29	46.8	111	7	US-11-056-355B-77101	Sequence 77101, A
258	29	46.8	117	7	US-11-056-355B-8460	Sequence 8460, Ap
259	29	46.8	118	6	US-10-953-349-40149	Sequence 40149, A
260	29	46.8	126	7	US-11-293-697-2488	Sequence 2488, Ap
261	29	46.8	137	7	US-11-056-355B-18725	Sequence 18725, A

262	29	46.8	141	6	US-10-449-902-32747	Sequence 32747, A
263	29	46.8	141	6	US-10-449-902-42618	Sequence 42618, A
264	29	46.8	156	7	US-11-056-355B-8459	Sequence 8459, Ap
265	29	46.8	157	7	US-11-056-355B-3255	Sequence 3255, Ap
266	29	46.8	167	7	US-11-056-355B-62943	Sequence 62943, A
267	29	46.8	168	7	US-11-340-003-19	Sequence 19, Appl
268	29	46.8	173	6	US-10-449-902-36023	Sequence 36023, A
269	29	46.8	173	6	US-10-449-902-43684	Sequence 43684, A
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271	29	46.8	177	7	US-11-056-355B-62942	Sequence 62942, A
272	29	46.8	190	7	US-11-340-003-21	Sequence 21, Appl
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274	29	46.8	196	6	US-10-953-349-32715	Sequence 32715, A
275	29	46.8	196	7	US-11-056-355B-56493	Sequence 56493, A
276	29	46.8	196	7	US-11-056-355B-63112	Sequence 63112, A
277	29	46.8	197	7	US-11-056-355B-75413	Sequence 75413, A
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281	29	46.8	212	7	US-11-056-355B-62941	Sequence 62941, A
282	29	46.8	217	6	US-10-449-902-38338	Sequence 38338, A
283	29	46.8	219	6	US-10-449-902-28919	Sequence 28919, A
284	29	46.8	219	6	US-10-449-902-45432	Sequence 45432, A
285	29	46.8	219	7	US-11-293-697-3175	Sequence 3175, Ap
286	29	46.8	225	6	US-10-953-349-35037	Sequence 35037, A
287	29	46.8	225	7	US-11-330-363-43	Sequence 43, Appl
288	29	46.8	225	7	US-11-056-355B-2775	Sequence 2775, Ap
289	29	46.8	229	6	US-10-953-349-24476	Sequence 24476, A
290	29	46.8	229	7	US-11-056-355B-57178	Sequence 57178, A
291	29	46.8	230	6	US-10-449-902-33533	Sequence 33533, A
292	29	46.8	230	6	US-10-449-902-45592	Sequence 45592, A
293	29	46.8	232	6	US-10-953-349-35036	Sequence 35036, A
294	29	46.8	232	7	US-11-056-355B-2774	Sequence 2774, Ap
295	29	46.8	233	6	US-10-449-902-48183	Sequence 48183, A
296	29	46.8	239	7	US-11-056-355B-107630	Sequence 107630, A
297	29	46.8	239	7	US-11-056-355B-118869	Sequence 118869, A
298	29	46.8	249	7	US-11-056-355B-38883	Sequence 38883, A
299	29	46.8	252	6	US-10-953-349-10036	Sequence 10036, A
300	29	46.8	252	7	US-11-056-355B-20347	Sequence 20347, A
301	29	46.8	261	7	US-11-056-355B-3830	Sequence 3830, Ap
302	29	46.8	262	7	US-11-056-355B-7163	Sequence 7163, Ap
303	29	46.8	266	7	US-11-056-355B-75412	Sequence 75412, A
304	29	46.8	273	6	US-10-953-349-15411	Sequence 15411, A
305	29	46.8	273	6	US-10-953-349-32714	Sequence 32714, A
306	29	46.8	273	7	US-11-056-355B-56492	Sequence 56492, A
307	29	46.8	273	7	US-11-056-355B-63111	Sequence 63111, A
308	29	46.8	296	7	US-11-056-355B-7162	Sequence 7162, Ap
309	29	46.8	298	6	US-10-953-349-30592	Sequence 30592, A
310	29	46.8	298	7	US-11-056-355B-63130	Sequence 63130, A
311	29	46.8	301	6	US-10-449-902-40123	Sequence 40123, A
312	29	46.8	306	6	US-10-449-902-56065	Sequence 56065, A
313	29	46.8	306	7	US-11-056-355B-1703	Sequence 1703, Ap
314	29	46.8	314	7	US-11-056-355B-7161	Sequence 7161, Ap
315	29	46.8	326	7	US-11-251-465-88	Sequence 88, Appl
316	29	46.8	326	7	US-11-056-355B-8599	Sequence 8599, Ap
317	29	46.8	331	6	US-10-449-902-50041	Sequence 50041, A
318	29	46.8	331	7	US-11-056-355B-100371	Sequence 100371, A
319	29	46.8	331	7	US-11-056-355B-111610	Sequence 111610, A
320	29	46.8	333	7	US-11-056-355B-100370	Sequence 100370, A
321	29	46.8	333	7	US-11-056-355B-111609	Sequence 111609, A
322	29	46.8	352	7	US-11-056-355B-8598	Sequence 8598, Ap
323	29	46.8	354	7	US-11-056-355B-20043	Sequence 20043, A
324	29	46.8	362	7	US-11-056-355B-6337	Sequence 6337, Ap
325	29	46.8	363	6	US-10-953-349-31676	Sequence 31676, A
326	29	46.8	363	7	US-11-056-355B-68550	Sequence 68550, A
327	29	46.8	366	7	US-11-056-355B-20042	Sequence 20042, A
328	29	46.8	371	6	US-10-449-902-35690	Sequence 35690, A
329	29	46.8	371	7	US-11-056-355B-14183	Sequence 14183, A
330	29	46.8	371	7	US-11-056-355B-19171	Sequence 19171, A
331	29	46.8	375	6	US-10-953-349-32145	Sequence 32145, A
332	29	46.8	375	7	US-11-056-355B-67768	Sequence 67768, A
333	29	46.8	384	6	US-10-449-902-37378	Sequence 37378, A
334	29	46.8	384	6	US-10-449-902-50064	Sequence 50064, A
335	29	46.8	393	6	US-10-449-902-37067	Sequence 37067, A
336	29	46.8	398	6	US-10-449-902-42308	Sequence 42308, A
337	29	46.8	406	6	US-10-953-349-14270	Sequence 14270, A
338	29	46.8	408	7	US-11-056-355B-8597	Sequence 8597, Ap
339	29	46.8	419	6	US-10-953-349-14269	Sequence 14269, A
340	29	46.8	441	6	US-10-953-349-31675	Sequence 31675, A
341	29	46.8	441	7	US-11-056-355B-68549	Sequence 68549, A
342	29	46.8	445	7	US-11-056-355B-100369	Sequence 100369, A

RESULT 35 B97661 probable transcription regulator (PA5428) [imported] - Agrobacterium tumefaciens (strain C5 Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanaga A;Molecule type: DNA A;Residues: 1-306 A;Cross-references: UNIPROT:Q8UCH5; UNIPARC:UPI00000D1F1F; GB GPLLRDLSAR 227 RESULT 36 S72817 probable glycoproteinase - Mycobacterium leprae N;Alternate names: B16 S72817 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-351 A;Cross-references: UNIPROT:P37969; L GPTIRCALAA 77 RESULT 37 H87480 conserved hypothetical protein CC1869 [imported] - Caulobacter crescentus B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, J.F.; Smit, J.; Craven. PMID:11259647 A;Accession: H87480 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-386 A;Cross-re Indels 0; Gaps 0; Qy 4 PTLRQXLAARA 14 | : | ||||| Db 318 PAIMQTLAARA 328 RESULT 38 S65358 familial Alzhei the dihydrofolate reductase gene in brain libraries derived from Alzheimer's disease patients. A;Reference numbe 4; Indels 0; Gaps 0; Qy 3 GPTLRQXLAAR 13 || || || | Db 374 GPDLSALAGR 384 RESULT 39 E87259 hypothetica Nelson, W.C.; Newton, A.; Stephens, C.; Phadke, N.D.; Ely, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: E87259 A;Status: pre 88.9%; Pred. No. 1.3e+02; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 6 LRQXLAARA 14 || Mujer, C.; Los, T.; Ivanova, N.; Anderson, I.; Bhattacharyya, A.; Lykidis, A.; Reznik, G.; Jablonski, L.; Larsen, N. PMID:11756688 A;Accession: AI3493 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-612 A;Cross-re Similarity 87.5%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 4 PTLRQX Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Pe A;Residues: 1-632 A;Cross-references: UNIPROT:Q92BZ0; UNIPARC:UPI00001299E5; GB:AL592022; PIDN:CAC! GPTLRQXLAA 12 |||| | | | Db 515 GPTLEQALKA 524 RESULT 42 PC4002 phosphatidylinositol-3 kinase (EC 3.1.3.- 678-682, 1995 A;Title: Phosphatidylinositol-3 kinase in fission yeast: A possible role in stress responses. A;Refer Score 34; DB 2; Length 664; Best Local Similarity 42.9%; Pred. No. 1.7e+02; Matches 6; Conservative 5; Misma C98069 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Estrem, S.; Fritz, L.; 5717, 2001 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Rosteck Jr., PIDN:AAL00384.1; PID:g15459247; GSPDB:GN00174 C;Genetics: A;Gene: priA Query Match 54.8%; Score 34; I Schizosaccharomyces pombe C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004 translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-801 A;Cross-references: UNIPROT:P5052I MUID:95290763; PMID:7772832 A;Accession: PC4002 A;Molecule type: DNA A;Residues: 138-163,'K',165-235,'I' internalization and delivery steps of endocytosis A;Note: specific for phosphatidylinositol, inactive on phosphatidy IEGPTLRQXLAARA 14 :|| :| :| :| Db 444 VEGRLIRETLAQA 457 RESULT 45 F75525 outer membrane protein - D. H.; Jiang, L.; Pamphile, W.; Crosby, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalev PMID:10567266 A;Accession: F75525 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-846 A;Cross-re Pred. No. 2.2e+02; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 5 TLRQXLAARA 14 | || ||||| novel vertebrate myosin I. A;Reference number: S31926 A;Accession: S31926 A;Status: preliminary A;Molecule domain homology F;110-117/Region: nucleotide-binding motif A (P-loop) F;1049-1096/Domain: SH3 homology C #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 C;Accession: A59300 R;Crozet, F.; Amraoui, A.E.; E A;Accession: A59300 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A; chain IB; myosin motor domain homology; SH3 homology F;20-677/Domain: myosin motor domain homology Qi A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #seque Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Fila PID:g17131737; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: all2644 C;Super 54.8%; Score 34; DB 2; Length 2617; Best Local Similarity 61.5%; Pred. No. 7.6e+02; Matches 8; Conservative submitted to the EMBL Data Library, November 1996 A;Reference number: Z19057 A;Accession: T18995 A;Statu 157/2; 288/2; 439/3; 542/1; 591/3; 798/3; 835/3; 1139/1; 1204/3; 1325/1; 1384/3; 1416/1; 1702/3; 1856/2; regulator PA3341 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Da Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Pa A;Residues: 1-144 A;Cross-references: UNIPROT:Q9HYQ4; UNIPARC:UPI00000C59C3; GB:AE004756; GB:AE004 VEGPTLARLL 71 Search completed: July 25, 2006, 09:44:31 Job time : 64 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 25, 2006, 09:38:53 ; Search time 39 Seconds
(without alignments)
37.006 Million cell updates/sec

Title: US-10-667-096-34
Perfect score: 62
Sequence: 1 IEGPTLRQXLAARAX 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result	% Query					
No.	Score	Match	Length	DB	ID	Description
1	40	64.5	246	2	AH0190	probable oxidoredu
2	40	64.5	400	2	C87021	serine-threonine p
3	38	61.3	664	2	H83962	serine/threonine p
4	37	59.7	491	2	C98275	polyketide synthas
5	37	59.7	491	2	AC3009	polyketide synthas
6	37	59.7	722	2	T37970	probable G2-specif
7	37	59.7	3172	2	S22012	erythronolide synt
8	37	59.7	3178	2	S13595	6-deoxyerythronoli
9	36.5	58.9	333	2	A36925	transcription acti
10	36	58.1	350	2	C87536	transcription regu
11	36	58.1	362	2	A64212	protein serine/thr
12	36	58.1	448	2	B45438	myosin I beta, MMI
13	36	58.1	698	2	T39050	hypothetical prote
14	36	58.1	807	2	H75634	myosin-Ic - mouse
15	36	58.1	1028	2	A59253	myosin I beta - hu
16	36	58.1	1028	2	S41749	myosin heavy chain
17	36	58.1	1028	2	S37146	myosin I heavy cha
18	35	56.5	274	2	H72521	probable thiazole
19	35	56.5	399	1	B70936	probable serine/th
20	35	56.5	478	2	AG0170	conserved hypothet
21	35	56.5	505	2	S68518	tub protein, brain
22	35	56.5	537	2	AE2454	two-component sens
23	35	56.5	584	2	C75364	probable long-chai
24	35	56.5	592	2	T42078	serine/threonine p
25	35	56.5	1203	2	H87687	helicase, UvrD/Rep
26	34.5	55.6	943	2	C82559	isoleucyl-tRNA syn
27	34	54.8	145	2	AG2706	conserved hypothet
28	34	54.8	148	2	AF0067	probable membrane
29	34	54.8	186	2	G97488	hypothetical prote
30	34	54.8	255	2	E75501	probable RNA methy
31	34	54.8	278	2	T45494	probable transposa
32	34	54.8	290	2	S72996	probable glycoprot
33	34	54.8	296	2	AG0147	probable membrane
34	34	54.8	306	2	AE2885	transcription regu
35	34	54.8	306	2	B97661	probable transcrip
36	34	54.8	351	2	S72817	probable glycoprot
37	34	54.8	386	2	H87480	conserved hypothet
38	34	54.8	440	2	S65358	familial Alzheimer
39	34	54.8	529	2	E87259	hypothetical prote
40	34	54.8	612	2	AI3493	oligopeptide-bindi
41	34	54.8	632	2	AI1607	D-1-deoxyxylulose
42	34	54.8	664	2	PC4002	phosphatidylinosit
43	34	54.8	798	2	C98069	primosomal replica
44	34	54.8	801	1	T52538	1-phosphatidylinos
45	34	54.8	846	2	F75525	outer membrane pro
46	34	54.8	1099	1	S31926	myosin IB heavy ch
47	34	54.8	1099	2	A59300	myosin-If - mouse
48	34	54.8	2617	2	AE2136	peptide synthetase
49	34	54.8	3036	2	T18995	hypothetical prote
50	33	53.2	144	2	G83228	probable transcrip
51	33	53.2	145	2	S07957	hypothetical prote
52	33	53.2	153	2	F70950	hypothetical prote

53	33	53.2	165	2	D87241	VPS29-like phospho
54	33	53.2	271	2	H83195	conserved hypothet
55	33	53.2	306	2	D70601	UTP-glucose-1-phos
56	33	53.2	311	2	F83047	conserved hypothet
57	33	53.2	336	2	T35643	glycerol-3-phospha
58	33	53.2	337	2	C75287	hypothetical prote
59	33	53.2	339	2	S47829	glycerol-3-phospha
60	33	53.2	339	2	G86036	glycerol-3-phospha
61	33	53.2	339	2	AB0975	glycerol-3-phospha
62	33	53.2	339	2	AD0009	glycerol-3-phospha
63	33	53.2	339	2	F91189	glycerol-3-phospha
64	33	53.2	342	2	S76463	hypothetical prote
65	33	53.2	344	2	AE2144	pyruvate dehydroge
66	33	53.2	344	2	H70737	probable o-sialogl
67	33	53.2	369	1	DEBSPF	pyruvate dehydroge
68	33	53.2	371	1	DEBSPA	pyruvate dehydroge
69	33	53.2	376	2	C87596	glycosyl hydrolase
70	33	53.2	389	2	S73910	probable serine/th
71	33	53.2	403	2	AD0748	tyrosine-specific
72	33	53.2	415	2	I39527	lambda integrase f
73	33	53.2	421	2	S26246	glutamate/aspartat
74	33	53.2	421	2	S26247	glutamate/aspartat
75	33	53.2	454	2	S16565	nolI protein - Rhi
76	33	53.2	489	2	AH0782	lysine-specific pe
77	33	53.2	499	2	C75251	phosphopyruvate hy
78	33	53.2	508	2	T37224	hypothetical prote
79	33	53.2	523	2	A83106	hypothetical prote
80	33	53.2	542	2	S42089	Rot(57) protein -
81	33	53.2	634	2	T00054	hypothetical prote
82	33	53.2	664	2	G89894	protein kinase [im
83	33	53.2	990	2	B49351	bacteriophage N4 a
84	33	53.2	990	2	H90703	bacteriophage N4 a
85	33	53.2	990	2	C85554	bacteriophage N4 a
86	33	53.2	1005	2	D95391	Probable cation ef
87	33	53.2	1014	2	JE0333	klotho protein - r
88	33	53.2	1021	2	T00361	hypothetical prote
89	33	53.2	1065	2	H95321	NolG efflux transp
90	33	53.2	1143	2	A69465	DNA-directed DNA p
91	33	53.2	1288	2	JE0363	mitogen-activated
92	33	53.2	1911	2	T43048	calcium channel al
93	32.5	52.4	388	2	H83438	probable aminotran
94	32.5	52.4	404	2	T36254	probable valine-py
95	32.5	52.4	4077	2	T17484	hypothetical prote
96	32	51.6	123	2	T45375	hypothetical prote
97	32	51.6	125	1	A46315	E4 protein - human
98	32	51.6	132	1	S15618	E4 protein - human
99	32	51.6	138	2	B23525	ribosomal protein
100	32	51.6	143	2	S31635	hypothetical prote
101	32	51.6	147	2	AB0126	conserved hypothet
102	32	51.6	150	2	H82150	conserved hypothet
103	32	51.6	157	2	A72662	hypothetical prote
104	32	51.6	167	2	S73026	hypothetical prote
105	32	51.6	170	1	NWMU2	2S albumin 2 precu
106	32	51.6	249	2	F75272	N-acetylglutamate
107	32	51.6	253	2	D72569	hypothetical prote
108	32	51.6	283	2	I45962	phenylethanolamine
109	32	51.6	284	1	A24313	phenylethanolamine
110	32	51.6	285	1	S38567	phenylethanolamine
111	32	51.6	301	2	H87515	polysaccharide dea
112	32	51.6	306	2	A72668	probable spermidin
113	32	51.6	330	1	F70590	hypothetical prote
114	32	51.6	330	2	C69593	3-methyl-2-oxobuta
115	32	51.6	349	2	B83118	hypothetical prote
116	32	51.6	352	2	F82343	conserved hypothet
117	32	51.6	373	2	A97426	flagellar P-ring p
118	32	51.6	373	2	AI2643	flagellar P-ring p
119	32	51.6	384	2	T37111	probable transcrip
120	32	51.6	393	2	AD0674	probable aminotran
121	32	51.6	401	2	H84483	hypothetical prote
122	32	51.6	404	2	D95233	aminotransferase,
123	32	51.6	404	2	F98097	aspartate transami
124	32	51.6	415	2	AF2894	glucosyltransferas
125	32	51.6	424	2	S12090	translation elonga
126	32	51.6	448	2	A97670	probable glycosylt
127	32	51.6	450	2	E98303	hypothetical 49.3K
128	32	51.6	450	2	AH2979	nitrilotriacetate
129	32	51.6	454	2	JC7231	thermophilic desul
130	32	51.6	459	2	S28025	light harvesting c
131	32	51.6	492	2	D37802	phytoene dehydroge
132	32	51.6	510	2	S77380	lysine-tRNA ligase
133	32	51.6	527	2	A75399	hypothetical prote

134	32	51.6	535	2	B70580	probable UDP-N-ace
135	32	51.6	540	2	A11050	probable acyl Co-A
136	32	51.6	546	2	S55386	cell fusion protei
137	32	51.6	549	2	JC5926	secreted klotho pr
138	32	51.6	597	2	AH2351	serine/threonine k
139	32	51.6	610	2	A96701	protein F12A21.3 [
140	32	51.6	649	2	S74823	N-acetylmuramoyl-L
141	32	51.6	696	2	T02832	long chain fatty a
142	32	51.6	818	2	T29560	hypothetical prote
143	32	51.6	888	2	JC5399	dual leucine zippe
144	32	51.6	888	2	A55318	serine/threonine p
145	32	51.6	943	2	T34847	probable transcrip
146	32	51.6	985	1	DJBIE11	DNA-directed DNA p
147	32	51.6	1012	2	JC5925	membrane klotho pr
148	32	51.6	1138	2	T36406	hypothetical prote
149	32	51.6	2529	2	B64635	toxin-like outer m
150	32	51.6	2591	2	T30288	pristinamycin I sy
151	31.5	50.8	269	2	JT0525	tryptophan synthas
152	31.5	50.8	310	2	H87058	L-asparaginase/L-g
153	31.5	50.8	409	2	T02776	y4dM protein - Rhi
154	31	50.0	92	2	PQ0632	coat protein - Rem
155	31	50.0	92	2	PQ0631	coat protein - lil
156	31	50.0	92	2	PQ0628	coat protein - tul
157	31	50.0	126	2	C95270	hypothetical prote
158	31	50.0	146	2	D90024	hypothetical prote
159	31	50.0	200	2	T23485	hypothetical prote
160	31	50.0	200	2	T45427	histone-like DNA b
161	31	50.0	201	1	BVECR	recombination prot
162	31	50.0	201	2	AI0562	recombination prot
163	31	50.0	201	2	A85545	recombination and
164	31	50.0	201	2	E90694	recombination prot
165	31	50.0	201	2	AI0378	recombination prot
166	31	50.0	207	2	T37464	probable glutathio
167	31	50.0	207	2	F75535	deoxyguanosine kin
168	31	50.0	209	2	E83224	conserved hypothet
169	31	50.0	225	2	G75448	conserved hypothet
170	31	50.0	253	2	D87679	hypothetical prote
171	31	50.0	264	2	A54060	nicotinamide N-met
172	31	50.0	264	2	S52102	thioether S-methyl
173	31	50.0	264	2	A44959	coat protein - pot
174	31	50.0	267	2	S26631	capsid protein - p
175	31	50.0	267	2	S14001	genome polyprotein
176	31	50.0	267	2	S26633	capsid protein - p
177	31	50.0	267	2	S26629	capsid protein - p
178	31	50.0	267	2	S26630	capsid protein - p
179	31	50.0	267	2	S26632	capsid protein - p
180	31	50.0	267	2	S26628	capsid protein - p
181	31	50.0	267	2	JC1527	coat protein - pot
182	31	50.0	267	2	A60924	coat protein - pot
183	31	50.0	267	2	A60366	coat protein - pot
184	31	50.0	268	2	D84849	hypothetical prote
185	31	50.0	269	2	JC1070	coat protein - pot
186	31	50.0	276	2	H70869	probable Enoyl-CoA
187	31	50.0	280	2	B45537	viral coat protein
188	31	50.0	284	2	S04723	genome polyprotein
189	31	50.0	292	2	G72530	probable nicotine
190	31	50.0	311	1	A40943	lactonizing lipase
191	31	50.0	311	1	S25768	triacylglycerol li
192	31	50.0	313	2	JT0960	polyprotein - pota
193	31	50.0	315	2	E84937	cysteine synthase
194	31	50.0	322	2	A64470	NADH dehydrogenase
195	31	50.0	324	2	B82641	transcription regu
196	31	50.0	325	2	AF3629	proteinase (EC 3.4
197	31	50.0	327	2	S11435	genome polyprotein
198	31	50.0	327	2	H87007	conserved hypothet
199	31	50.0	330	2	A26205	coat protein precu
200	31	50.0	331	2	AD1246	branched-chain alp
201	31	50.0	331	2	AH1608	branched-chain alp
202	31	50.0	332	2	C96693	hypothetical prote
203	31	50.0	336	2	A47542	short-chain alchoh
204	31	50.0	356	2	S45330	thrombopoietin - m
205	31	50.0	365	2	E82585	histidinol-phospha
206	31	50.0	371	2	AD1206	pyruvate dehydroge
207	31	50.0	371	2	AC1563	pyruvate dehydroge
208	31	50.0	377	2	F95982	probable transport
209	31	50.0	379	2	S13556	genome polyprotein
210	31	50.0	381	2	S14132	orotidine-5'-phosp
211	31	50.0	381	2	F87553	aminotransferase,
212	31	50.0	382	2	B86575	hypothetical prote
213	31	50.0	382	2	A72049	hypothetical prote
214	31	50.0	386	2	B82921	serine/threonine k

215	31	50.0	387	2	B84313	aminomethyltransfe
216	31	50.0	391	2	T25826	hypothetical prote
217	31	50.0	392	2	A44167	aminomethyltransfe
218	31	50.0	393	2	JQ0461	genome polyprotein
219	31	50.0	397	2	A23707	aminomethyltransfe
220	31	50.0	402	2	S23774	triose phosphate/3
221	31	50.0	403	2	I54192	aminomethyltransfe
222	31	50.0	415	2	T35834	probable transcrip
223	31	50.0	416	2	E87286	3-deoxy-D-manno-oc
224	31	50.0	423	2	S58191	genome polyprotein
225	31	50.0	424	2	T07742	omega-6 desaturase
226	31	50.0	424	2	T25774	hypothetical prote
227	31	50.0	427	2	JA0073	genome polyprotein
228	31	50.0	431	2	B75491	proton/sodium-glut
229	31	50.0	434	2	F84332	succinoglycan bios
230	31	50.0	436	2	T09963	mitosis-specific c
231	31	50.0	436	2	AC1021	proton glutamate s
232	31	50.0	437	2	A42384	glutamate-aspartat
233	31	50.0	437	2	C91261	glutamate-aspartat
234	31	50.0	437	2	G86101	glutamate-aspartat
235	31	50.0	438	2	AH0031	proton glutamate s
236	31	50.0	444	2	A82962	proton-glutamate s
237	31	50.0	449	2	JQ1438	polyprotein - tuli
238	31	50.0	480	2	T24087	hypothetical prote
239	31	50.0	489	1	C64984	lysine-specific pe
240	31	50.0	489	2	H91009	lysine-specific pe
241	31	50.0	489	2	B85854	lysine-specific pe
242	31	50.0	504	2	H70520	hypothetical glyci
243	31	50.0	510	2	H83197	probable hydroxyac
244	31	50.0	517	2	S32169	hypothetical prote
245	31	50.0	525	2	G75527	lysyl-tRNA synthet
246	31	50.0	526	2	F83166	hypothetical prote
247	31	50.0	533	2	S43526	amidophosphoribosy
248	31	50.0	536	1	SYECEB	2,3-dihydroxybenzo
249	31	50.0	536	2	E85558	2,3-dihydroxybenzo
250	31	50.0	536	2	A99708	2,3-dihydroxybenzo
251	31	50.0	546	2	AC2269	serine/threonine k
252	31	50.0	609	1	A42537	gene 16 protein -
253	31	50.0	643	2	S36563	E1 protein - human
254	31	50.0	675	2	G85582	probable proteinase
255	31	50.0	695	2	B75295	hypothetical prote
256	31	50.0	707	2	E90732	probable proteinase
257	31	50.0	739	2	T45429	polyphosphate kina
258	31	50.0	742	2	E70673	probable ppk prote
259	31	50.0	749	2	C87618	excinuclease ABC,
260	31	50.0	787	2	S72725	guanosine-3',5'bis
261	31	50.0	790	2	F70725	probable relA prot
262	31	50.0	791	2	S61698	hypothetical prote
263	31	50.0	813	2	B47485	ABR protein 2 - hu
264	31	50.0	813	2	T31214	hypothetical prote
265	31	50.0	831	2	G87620	TonB-dependent rec
266	31	50.0	837	2	H82970	hypothetical prote
267	31	50.0	838	2	A32262	fatty-acid synthas
268	31	50.0	846	2	A60678	genome polyprotein
269	31	50.0	859	2	A49307	98K GTPase-activat
270	31	50.0	959	1	B71405	probable kinesin -
271	31	50.0	1008	2	S38003	translation elonga
272	31	50.0	1019	2	T11560	pol polyprotein -
273	31	50.0	1100	2	AF1460	alpha-xylosidase a
274	31	50.0	1100	2	AG1097	alpha-xylosidase a
275	31	50.0	1132	2	S37206	phytochrome - moss
276	31	50.0	1218	2	A88429	protein C28A5.2 [i
277	31	50.0	1293	1	YGECF	enterobactin synth
278	31	50.0	1293	2	E85557	enterobactin synth
279	31	50.0	1293	2	A90707	enterobactin synth
280	31	50.0	1294	2	AP0574	enterobactin synth
281	31	50.0	1521	2	S35241	emb-5 protein - Ca
282	31	50.0	1555	2	JT0959	polyprotein - pota
283	31	50.0	1689	2	S72467	sodium channel pro
284	31	50.0	1770	2	T18551	saframycin Mx1 syn
285	31	50.0	1875	2	A36429	integrin beta-4 ch
286	31	50.0	1888	2	T14273	zinc finger protei
287	31	50.0	2429	1	SJHUA	spectrin alpha cha
288	31	50.0	3061	1	JN0545	genome polyprotein
289	31	50.0	3063	2	JS0166	genome polyprotein
290	30.5	49.2	151	1	GGNKT	globin beta chain
291	30.5	49.2	151	2	S09068	hemoglobin IIb - a
292	30.5	49.2	242	2	A82637	conserved hypothet
293	30.5	49.2	526	2	D75391	AlgP-related prote
294	30.5	49.2	710	1	S70965	serine/threonine-s
295	30.5	49.2	1148	2	AD0198	transcription-repa

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OM protein - protein search, using sw model

Run on: July 25, 2006, 09:36:58 ; Search time 295 Seconds
(without alignments)
47.035 Million cell updates/sec

Title: US-10-667-096-34
Perfect score: 62
Sequence: 1 IEGPTLRQXLAARAX 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	45	72.6	325	2	Q855N9_9CAUD Q855n9 mycobacteri
2	43	69.4	531	2	Q3VY76_9ACTO Q3vy76 frankia sp.
3	43	69.4	554	2	Q2T740_BURTH Q2t740 burkholderi
4	42	67.7	298	2	Q3QST4_9RHOB Q3qst4 silicibacte
5	42	67.7	544	2	Q446W0_SOLUS Q446w0 solibacter
6	41	66.1	353	2	Q9KWU0_9SPHN Q9kwu0 sphingomona
7	40	64.5	246	2	Q66C35_YERPS Q66c35 yersinia ps
8	40	64.5	246	2	Q8ZFW2_YERPE Q8zfw2 yersinia pe
9	40	64.5	400	2	Q69568_MYCLE Q69568 mycobacteri
10	40	64.5	472	2	Q3KCE1_PSEPF Q3kce1 pseudomonas
11	40	64.5	476	2	Q44J21_CHRSL Q44j21 chromohalob
12	40	64.5	519	2	Q3ANJ4_SYNSC Q3anj4 synechococc
13	40	64.5	3308	2	Q3MCQ2_ANAVT Q3mcq2 anabaena va
14	39	62.9	165	2	Q30UR0_DESDG Q30ur0 desulfovibr
15	39	62.9	227	2	Q9RBZ4_PSESG Q9rbz4 pseudomonas
16	39	62.9	227	2	Q88BV4_PSESM Q88bv4 pseudomonas
17	39	62.9	268	2	Q98LG1_RHILO Q98lg1 rhizobium l
18	39	62.9	352	2	Q67DX1_9RALS Q67dx1 ralstonia s
19	39	62.9	502	2	Q82LK6_STRAW Q82lk6 streptomyce
20	39	62.9	505	2	Q8DGC3_SYNEL Q8dgc3 synechococc
21	39	62.9	551	2	Q67QP4_SYMTH Q67qp4 symbiobacte
22	39	62.9	759	2	Q2JMW5_9CYAN Q2jm75 cyanobacter
23	39	62.9	1124	2	Q2J6J7_9ACTO Q2j6j7 frankia sp.
24	38	61.3	27	2	Q9GU44_9METZ Q9gu44 sycon rapha

25	38	61.3	27	2	Q9GU45_9METZ	Q9gu45 sycon rapha
26	38	61.3	175	2	Q69MK4_ORYSA	Q69mk4 oryza sativ
27	38	61.3	379	2	Q5LP04_SILPO	Q5lp04 silicibacte
28	38	61.3	386	2	Q2UMG7_ASPOR	Q2umg7 aspergillus
29	38	61.3	398	2	Q3K8U8_PSEPP	Q3k8u8 pseudomonas
30	38	61.3	415	2	Q4K4Y7_PSEF5	Q4k4y7 pseudomonas
31	38	61.3	429	2	Q4NA44_9MICC	Q4na44 arthrobacte
32	38	61.3	441	2	Q73S55_MYCPA	Q73s55 mycobacteri
33	38	61.3	664	2	Q9K9Z0_BACHD	Q9k9z0 bacillus ha
34	38	61.3	812	2	Q3WD36_9ACTO	Q3wd36 frankia sp.
35	38	61.3	883	2	Q44CM3_CHRSL	Q44cm3 chromohalob
36	38	61.3	947	2	Q69Z49_MOUSE	Q69z49 mus musculu
37	38	61.3	994	2	Q6DFU9_MOUSE	Q6dfu9 mus musculu
38	38	61.3	1096	2	Q2ZUQ8_SHEPU	Q2zuq8 shewanella
39	38	61.3	1228	2	Q3UPD8_MOUSE	Q3upd8 mus musculu
40	38	61.3	1241	2	Q9HfY7_COLGL	Q9hfy7 colletotric
41	38	61.3	1289	1	S3TC2_MOUSE	Q80va5 mus musculu
42	38	61.3	2987	2	Q7QWR0_GIALA	Q7qwr0 giardia lam
43	37	59.7	53	2	Q5YWJ5_NOCFA	Q5ywj5 nocardia fa
44	37	59.7	134	2	Q5LF77_BACFN	Q5lf77 bacteroides
45	37	59.7	175	2	Q92KP6_RHIME	Q92kp6 rhizobium m
46	37	59.7	180	2	Q3J4B1_RHOS4	Q3j4b1 rhodobacter
47	37	59.7	194	2	Q72JS0_THET2	Q72js0 thermus the
48	37	59.7	210	2	Q44FR1_CHRSL	Q44fr1 chromohalob
49	37	59.7	219	2	Q4P4Y5_USTMA	Q4p4y5 ustilago ma
50	37	59.7	229	2	Q3AZ50_SYNS9	Q3az50 synechococc
51	37	59.7	238	2	Q9LTX0_ARATH	Q9ltx0 arabidopsis
52	37	59.7	244	2	Q8PPV5_XANAC	Q8ppv5 xanthomonas
53	37	59.7	295	2	Q8Y2M4_RALSO	Q8y2m4 ralstonia s
54	37	59.7	302	2	Q742B3_MYCPA	Q742b3 mycobacteri
55	37	59.7	323	2	Q4CYK7_TRYCR	Q4cyk7 trypanosoma
56	37	59.7	348	2	Q3P9G9_PARDE	Q3p9g9 paracoccus
57	37	59.7	358	2	Q2YCG0_NITMU	Q2ycg0 nitrosospir
58	37	59.7	392	2	Q2XE52_PSEPU	Q2xe52 pseudomonas
59	37	59.7	392	2	Q88NB4_PSEPK	Q88nb4 pseudomonas
60	37	59.7	398	2	Q740W3_MYCPA	Q740w3 mycobacteri
61	37	59.7	457	2	Q3X4X7_9ACTN	Q3x4x7 rubrobacter
62	37	59.7	472	2	Q3P7I9_PARDE	Q3p7i9 paracoccus
63	37	59.7	491	2	Q8U9P9_AGR5	Q8u9p9 agrobacteri
64	37	59.7	514	2	Q2U4P0_ASPOR	Q2u4p0 aspergillus
65	37	59.7	558	2	Q4D731_TRYCR	Q4d731 trypanosoma
66	37	59.7	559	2	Q5SK77_THET8	Q5sk77 thermus the
67	37	59.7	608	2	Q2KGN7_MAGGR	Q2kg7 magnaporthe
68	37	59.7	608	2	Q46SU3_RALEJ	Q46su3 ralstonia e
69	37	59.7	610	2	Q2UF05_ASPOR	Q2uf05 aspergillus
70	37	59.7	642	2	Q4V834_XENLA	Q4v834 xenopus lae
71	37	59.7	647	2	Q7ZWR1_XENLA	Q7zwr1 xenopus lae
72	37	59.7	707	1	DP13A_MOUSE	Q8k3h0 mus musculu
73	37	59.7	707	2	Q3UJP7_MOUSE	Q3ujp7 mus musculu
74	37	59.7	708	2	Q6P9I3_XENLA	Q6p9i3 xenopus lae
75	37	59.7	709	1	DP13A_HUMAN	Q9ukg1 homo sapien
76	37	59.7	722	1	FIN1_SCHPO	O13839 schizosacch
77	37	59.7	741	2	Q4RIF7_TETNG	Q4rif7 tetraodon n
78	37	59.7	776	2	Q4ST67_TETNG	Q4st67 tetraodon n
79	37	59.7	828	2	Q2J7X9_9ACTO	Q2j7x9 frankia sp.
80	37	59.7	1896	2	Q9DRA1_9VIRU	Q9dra1 botrytis vi
81	37	59.7	3171	1	ERYA3_SACER	Q03133 saccharopol
82	37	59.7	3171	2	Q5UNP4_SACER	Q5unp4 saccharopol
83	37	59.7	3314	2	Q2KX68_BORAV	Q2kx68 bordetella
84	36.5	58.9	333	1	CBBR_XANFL	P25545 xanthobacte
85	36	58.1	81	2	Q2PZS6_HUMAN	Q2pzs6 homo sapien
86	36	58.1	129	2	Q7QTQ5_GIALA	Q7qtq5 giardia lam
87	36	58.1	141	2	Q93L35_RHILV	Q93l35 rhizobium l
88	36	58.1	150	2	Q3RVB8_RALME	Q3rvb8 ralstonia m
89	36	58.1	208	2	Q314Y7_DESDG	Q314y7 desulfovibr
90	36	58.1	226	2	Q4AUU7_9BURK	Q4auu7 polaromonas
91	36	58.1	232	2	Q53LM9_ORYSA	Q53lm9 oryza sativ
92	36	58.1	248	2	Q3C5H0_9CLOT	Q3c5h0 alkaliphilu
93	36	58.1	258	2	Q982J8_RHILO	Q982j8 rhizobium l
94	36	58.1	260	2	Q5LT94_SILPO	Q5lt94 silicibacte
95	36	58.1	261	2	Q44I90_CHRSL	Q44i90 chromohalob
96	36	58.1	264	2	Q3VYT1_9ACTO	Q3vyt1 frankia sp.
97	36	58.1	265	2	Q35H34_9BRAD	Q35h34 bradyrhizob
98	36	58.1	265	2	Q35P56_9BRAD	Q35p56 bradyrhizob
99	36	58.1	265	2	Q3FD28_9BURK	Q3fd28 burkholderi
100	36	58.1	265	2	Q3RZQ9_RALME	Q3rzq9 ralstonia m
101	36	58.1	265	2	Q3JG14_BURP1	Q3jg14 burkholderi
102	36	58.1	265	2	Q2IFD3_9DELT	Q2ifd3 anaeromyxob
103	36	58.1	265	2	Q62D62_BURMA	Q62d62 burkholderi
104	36	58.1	265	2	Q63M96_BURPS	Q63m96 burkholderi
105	36	58.1	268	2	Q45AU8_9BURK	Q45au8 burkholderi

106	36	58.1	268	2	Q4LTV5_9BURK	Q4ltv5 burkholderi
107	36	58.1	273	2	Q72EA3_DESVH	Q72ea3 desulfovibr
108	36	58.1	286	1	SPEE_PROMM	Q7v3x3 prochloroco
109	36	58.1	319	2	Q9RKM5_STRCO	Q9rkm5 streptomyce
110	36	58.1	328	2	Q3IHC0_PSEHT	Q3ihc0 pseudoalter
111	36	58.1	329	2	Q98J88_RHILO	Q98j88 rhizobium l
112	36	58.1	331	2	Q606L9_METCA	Q606l9 methylococc
113	36	58.1	332	2	Q3J1Y8_RHOS4	Q3jly8 rhodobacter
114	36	58.1	344	2	Q9ADF6_STRCO	Q9adf6 streptomyce
115	36	58.1	345	2	Q82L89_STRAW	Q82l89 streptomyce
116	36	58.1	345	2	Q9L0R7_STRCO	Q9l0r7 streptomyce
117	36	58.1	350	2	Q9A5Y1_CAUCR	Q9a5y1 caulobacter
118	36	58.1	358	2	Q6IQM4_BRARE	Q6iqm4 brachydanio
119	36	58.1	374	2	Q73S53_MYCPA	Q73s53 mycobacteri
120	36	58.1	382	2	Q2RXQ1_RHORU	Q2rxq1 rhodospiril
121	36	58.1	387	1	PKNS_MYCGE	P47355 mycoplasma
122	36	58.1	396	2	Q73YP1_MYCPA	Q73yp1 mycobacteri
123	36	58.1	397	2	Q59EP6_HUMAN	Q59ep6 homo sapien
124	36	58.1	413	2	Q397C0_BURS3	Q397c0 burkholderi
125	36	58.1	431	2	Q4NC85_9MICC	Q4nc85 arthrobacte
126	36	58.1	432	2	Q4R3P8_MACFA	Q4r3p8 macaca fasc
127	36	58.1	439	2	Q2KWS6_BORAV	Q2kws6 bordetella
128	36	58.1	440	2	Q8S838_ORYSA	Q8s838 oryza sativ
129	36	58.1	491	2	O76269_LEIDO	O76269 leishmania
130	36	58.1	491	2	O76343_LEIDO	O76343 leishmania
131	36	58.1	491	2	Q4QF58_LEIMA	Q4qf58 leishmania
132	36	58.1	502	2	Q5YMV8_NOCFA	Q5ymv8 nocardia fa
133	36	58.1	511	2	Q2X9A4_PSEPU	Q2x9a4 pseudomonas
134	36	58.1	523	2	Q2IDV6_9DELT	Q2idv6 anaeromyxob
135	36	58.1	554	2	Q3JKY9_BURP1	Q3jky9 burkholderi
136	36	58.1	554	2	Q62AX8_BURMA	Q62ax8 burkholderi
137	36	58.1	554	2	Q63K05_BURPS	Q63k05 burkholderi
138	36	58.1	562	2	Q5YN92_NOCFA	Q5yn92 nocardia fa
139	36	58.1	566	2	Q4R8K9_MACFA	Q4r8k9 macaca fasc
140	36	58.1	569	2	Q2YBC6_NITMU	Q2ybc6 nitrospir
141	36	58.1	583	2	Q43LG7_SOLUS	Q43lg7 solibacter
142	36	58.1	584	2	Q55NM2_CRYNE	Q55nm2 cryptococcu
143	36	58.1	586	2	Q5KC10_CRYNE	Q5kc10 cryptococcu
144	36	58.1	604	2	Q98P10_RHILO	Q98p10 rhizobium l
145	36	58.1	605	1	MBD1_HUMAN	Q9uis9 homo sapien
146	36	58.1	620	2	Q7XWI5_ORYSA	Q7xwi5 oryza sativ
147	36	58.1	656	2	Q4QF59_LEIMA	Q4qf59 leishmania
148	36	58.1	668	2	Q3IWK6_RHOS4	Q3iwk6 rhodobacter
149	36	58.1	691	2	Q2W0M9_MAGSA	Q2w0m9 magnetospir
150	36	58.1	692	2	Q4QCU8_LEIMA	Q4qcu8 leishmania
151	36	58.1	692	2	Q3BQ33_XANC5	Q3bq33 xanthomonas
152	36	58.1	796	2	Q9RL24_STRCO	Q9rl24 streptomyce
153	36	58.1	802	2	Q3FCP9_9BURK	Q3fcp9 burkholderi
154	36	58.1	802	2	Q3T1L0_RAT	Q3t1l0 rattus norv
155	36	58.1	806	2	Q3X9C3_METFL	Q3x9c3 methylobaci
156	36	58.1	835	2	Q2J8N3_9ACTO	Q2j8n3 frankia sp.
157	36	58.1	913	2	Q584Z8_9TRYP	Q584z8 trypanosoma
158	36	58.1	964	2	Q4IJA7_GIBZE	Q4ija7 gibberella
159	36	58.1	967	2	Q8A3E8_BACTN	Q8a3e8 bacteroides
160	36	58.1	991	2	Q3TBQ4_MOUSE	Q3tbq4 mus musculu
161	36	58.1	1028	1	MYO1C_BOVIN	Q27966 bos taurus
162	36	58.1	1028	1	MYO1C_HUMAN	O00159 homo sapien
163	36	58.1	1028	1	MYO1C_MOUSE	Q9wti7 mus musculu
164	36	58.1	1028	2	Q6NVJ7_HUMAN	Q6nvj7 homo sapien
165	36	58.1	1028	2	Q3U231_MOUSE	Q3u231 mus musculu
166	36	58.1	1028	2	Q5ND49_MOUSE	Q5nd49 mus musculu
167	36	58.1	1028	2	Q63355_RAT	Q63355 rattus norv
168	36	58.1	1030	2	Q86Y95_HUMAN	Q86y95 homo sapien
169	36	58.1	1044	2	Q9ERB6_MOUSE	Q9erb6 mus musculu
170	36	58.1	1078	2	Q8LLX9_ORYSA	Q8llx9 oryza sativ
171	36	58.1	1088	2	Q339Y4_ORYSA	Q339y4 oryza sativ
172	36	58.1	1097	2	Q4LE56_HUMAN	Q4le56 homo sapien
173	36	58.1	1279	2	Q2R6H5_ORYSA	Q2r6h5 oryza sativ
174	36	58.1	1337	2	Q53KQ8_ORYSA	Q53kq8 oryza sativ
175	36	58.1	1361	2	Q3XNY0_9PROT	Q3xny0 magnetococc
176	36	58.1	1383	2	Q2R4N6_ORYSA	Q2r4n6 oryza sativ
177	36	58.1	1398	2	Q53JS3_ORYSA	Q53js3 oryza sativ
178	36	58.1	1400	1	RIF1_SCHPO	Q96up3 schizosacch
179	36	58.1	1416	2	Q7G654_ORYSA	Q7g654 oryza sativ
180	36	58.1	1416	2	Q8W5E8_ORYSA	Q8w5e8 oryza sativ
181	36	58.1	1456	2	Q5H9W5_ORYSA	Q5h9w5 oryza sativ
182	36	58.1	1467	2	Q7XWU5_ORYSA	Q7xwu5 oryza sativ
183	36	58.1	1473	2	Q8H8R0_ORYSA	Q8h8r0 oryza sativ
184	36	58.1	1473	2	Q94H22_ORYSA	Q94h22 oryza sativ
185	36	58.1	1476	2	Q7XS24_ORYSA	Q7xs24 oryza sativ
186	36	58.1	1480	2	Q7XLJ7_ORYSA	Q7xlj7 oryza sativ

187	36	58.1	1484	2	Q7XM70_ORYSA	Q7xm70 oryza sativ
188	36	58.1	1496	2	Q8S760_ORYSA	Q8s760 oryza sativ
189	36	58.1	1523	2	Q8LM00_ORYSA	Q8lm00 oryza sativ
190	36	58.1	1529	2	Q2R8S5_ORYSA	Q2r8s5 oryza sativ
191	36	58.1	1530	2	Q53J71_ORYSA	Q53j71 oryza sativ
192	36	58.1	1535	2	Q53N07_ORYSA	Q53n07 oryza sativ
193	36	58.1	1543	2	Q33AQ9_ORYSA	Q33aq9 oryza sativ
194	36	58.1	1550	2	Q2QPZ1_ORYSA	Q2qpz1 oryza sativ
195	36	58.1	1564	2	Q7Y0A9_ORYSA	Q7y0a9 oryza sativ
196	36	58.1	1569	2	Q53J31_ORYSA	Q53j31 oryza sativ
197	36	58.1	1594	2	Q5W6A7_ORYSA	Q5w6a7 oryza sativ
198	36	58.1	1594	2	Q7XFS6_ORYSA	Q7xf6s oryza sativ
199	36	58.1	1594	2	Q8S782_ORYSA	Q8s782 oryza sativ
200	36	58.1	1596	2	Q339Z4_ORYSA	Q339z4 oryza sativ
201	36	58.1	1607	2	Q2QRY4_ORYSA	Q2qry4 oryza sativ
202	36	58.1	1625	2	Q7XR40_ORYSA	Q7xr40 oryza sativ
203	36	58.1	1645	2	Q2QPF5_ORYSA	Q2qpf5 oryza sativ
204	36	58.1	1646	2	Q7WTE3_9ACTO	Q7wte3 streptomyce
205	36	58.1	1652	2	Q84SQ8_ORYSA	Q84sq8 oryza sativ
206	36	58.1	1686	2	Q53KP3_ORYSA	Q53kp3 oryza sativ
207	36	58.1	1699	2	Q2QRA7_ORYSA	Q2qra7 oryza sativ
208	36	58.1	1762	2	Q2R2J9_ORYSA	Q2r2j9 oryza sativ
209	36	58.1	1770	2	Q851D3_ORYSA	Q851d3 oryza sativ
210	36	58.1	1847	2	Q53N03_ORYSA	Q53n03 oryza sativ
211	36	58.1	1922	2	Q4UAX6_THEAN	Q4uax6 theileria a
212	36	58.1	2221	2	Q5AV42_EMENI	Q5av42 aspergillus
213	36	58.1	3092	2	Q5WMN7_ORYSA	Q5wmn7 oryza sativ
214	36	58.1	3268	2	Q2IG57_9DELT	Q2ig57 anaeromyxob
215	36	58.1	6274	2	Q3JS97_BURP1	Q3js97 burkholderi
216	36	58.1	6274	2	Q63UA4_BURPS	Q63ua4 burkholderi
217	36	58.1	6889	2	Q8XS40_RALSO	Q8xs40 ralstonia s
218	35.5	57.3	555	2	Q7QHJ7_ANOGA	Q7qhj7 anopheles g
219	35.5	57.3	874	1	GLND_PHOPR	Q6ln22 photobacter
220	35.5	57.3	874	1	GLND_VIBPA	Q87md6 vibrio para
221	35	56.5	61	2	Q5YS14_NOCFA	Q5ys14 nocardia fa
222	35	56.5	75	2	Q3ESD1_CHLAU	Q3e5d1 chloroflexu
223	35	56.5	79	2	Q3ITH5_NATPD	Q3ith5 natronomona
224	35	56.5	93	2	Q89US7_BRAJA	Q89us7 bradyrhizob
225	35	56.5	126	2	Q2NP78_9CAUD	Q2np78 xanthomonas
226	35	56.5	133	2	Q7S3L9_NEUCR	Q7s3l9 neurospora
227	35	56.5	141	2	Q2K5B3_RHIET	Q2k5b3 rhizobium e
228	35	56.5	143	1	H2AV_NEUCR	Q873g4 neurospora
229	35	56.5	143	2	Q2L3E3_BRASY	Q2l3e3 brachypodiu
230	35	56.5	165	2	Q36TP7_MARHY	Q36tp7 marinobacte
231	35	56.5	175	2	Q9L455_9ACTO	Q9l455 propionibac
232	35	56.5	178	2	Q7U3P6_SYNXP	Q7u3p6 synechococc
233	35	56.5	179	2	Q6L3H9_SOLDE	Q6l3h9 solanum dem
234	35	56.5	179	2	Q2INR5_9DELT	Q2inr5 anaeromyxob
235	35	56.5	184	2	Q7NQ79_CHRVO	Q7nq79 chromobacte
236	35	56.5	216	2	Q6K5R3_ORYSA	Q6k5r3 oryza sativ
237	35	56.5	225	2	Q3AHF8_SYNSC	Q3ahf8 synechococc
238	35	56.5	229	2	Q8XXT3_RALSO	Q8xxt3 ralstonia s
239	35	56.5	240	2	Q72NC8_LEPIC	Q72nc8 leptospira
240	35	56.5	240	2	Q8F863_LEPIN	Q8f863 leptospira
241	35	56.5	244	2	Q69MD4_ORYSA	Q69md4 oryza sativ
242	35	56.5	246	2	Q3HKF0_RHOS4	Q3hkf0 rhodobacter
243	35	56.5	246	2	Q3PE76_PARDE	Q3pe76 paracoccus
244	35	56.5	248	2	Q5LNS7_SILPO	Q5lns7 silicibacte
245	35	56.5	254	2	Q3F716_9BURK	Q3f716 burkholderi
246	35	56.5	258	2	Q3PA42_PARDE	Q3pa42 paracoccus
247	35	56.5	264	2	Q46WB2_RALEJ	Q46wb2 ralstonia e
248	35	56.5	264	2	Q8PPF9_XANAC	Q8ppf9 xanthomonas
249	35	56.5	271	2	Q6L456_SOLDE	Q6l456 solanum dem
250	35	56.5	274	1	THI4_AERPE	Q9y9z0 aeropyrum p
251	35	56.5	276	2	Q827H0_STRAW	Q827h0 streptomyce
252	35	56.5	277	2	Q3JTD5_BURP1	Q3jtd5 burkholderi
253	35	56.5	277	2	Q63TB8_BURPS	Q63tb8 burkholderi
254	35	56.5	281	2	Q3FBX7_9BURK	Q3fbx7 burkholderi
255	35	56.5	281	2	Q3WD58_9ACTO	Q3wd58 frankia sp.
256	35	56.5	281	2	Q44U28_9BURK	Q44u28 burkholderi
257	35	56.5	281	2	Q4LJ28_9BURK	Q4lj28 burkholderi
258	35	56.5	304	2	Q7S6Q9_NEUCR	Q7s6q9 neurospora
259	35	56.5	307	2	Q2IF19_9DELT	Q2if19 anaeromyxob
260	35	56.5	311	2	Q7EYC9_ORYSA	Q7eyc9 oryza sativ
261	35	56.5	314	2	Q3XW17_9PROT	Q3xw17 magnetococc
262	35	56.5	321	2	Q46Y21_RALEJ	Q46y21 ralstonia e
263	35	56.5	324	2	Q47I18_DECAR	Q47i18 dechloromon
264	35	56.5	338	2	Q46UI0_RALEJ	Q46ui0 ralstonia e
265	35	56.5	340	2	Q2QSE2_ORYSA	Q2qse2 oryza sativ
266	35	56.5	341	2	Q73S13_MYCPA	Q73s13 mycobacteri
267	35	56.5	344	2	Q9RJR6_STRCO	Q9rjr6 streptomyce

268	35	56.5	354	2	Q2NGL1_9EURY	Q2ngl1	methanospha
269	35	56.5	362	2	Q3J2H5_RHOS4	Q3j2h5	rhodobacter
270	35	56.5	369	2	Q8ZYE4_PYRAE	Q8zye4	pyrobaculum
271	35	56.5	373	2	Q96JS0_HUMAN	Q96js0	homo sapien
272	35	56.5	389	2	Q2JDT8_9ACTO	Q2jdt8	frankia sp.
273	35	56.5	392	2	Q62FP5_BURMA	Q62fp5	burkholderi
274	35	56.5	392	2	Q63PK0_BURPS	Q63pk0	burkholderi
275	35	56.5	392	2	Q6N7B2_RHOPA	Q6n7b2	rhodopseudo
276	35	56.5	399	1	PKNL_MYCBO	Q7tyy6	mycobacteri
277	35	56.5	399	1	PKNL_MYCTU	O53510	mycobacteri
278	35	56.5	403	2	Q7WBY0_BORPA	Q7wby0	bordetella
279	35	56.5	403	2	Q7WPX6_BORBR	Q7wp6	bordetella
280	35	56.5	406	2	Q3W5T2_9ACTO	Q3w5t2	frankia sp.
281	35	56.5	408	2	Q3E3R5_CHLAU	Q3e3r5	chloroflexu
282	35	56.5	411	2	Q46V73_RALEJ	Q46v73	ralstonia e
283	35	56.5	412	2	Q455J1_9BURK	Q455j1	burkholderi
284	35	56.5	412	2	Q4LLD9_9BURK	Q4lld9	burkholderi
285	35	56.5	419	2	Q9D4K7_MOUSE	Q9d4k7	mus musculu
286	35	56.5	420	2	Q9H4D2_HUMAN	Q9h4d2	homo sapien
287	35	56.5	422	2	Q67KG4_SYMTH	Q67kg4	symbiobacte
288	35	56.5	430	2	Q2N2P8_AERHY	Q2n2p8	aeromonas h
289	35	56.5	435	2	Q419I1_KINRA	Q419i1	kineococcus
290	35	56.5	435	2	Q3JXZ3_BURP1	Q3jxz3	burkholderi
291	35	56.5	441	2	Q35IK9_9BRAD	Q35ik9	bradyrhizob
292	35	56.5	457	2	Q35NM5_9BRAD	Q35nm5	bradyrhizob
293	35	56.5	472	2	Q74VT4_YERPE	Q74vt4	yersinia pe
294	35	56.5	473	2	Q8T8Z0_DROME	Q8t8z0	drosophila
295	35	56.5	473	2	Q9VJH7_DROME	Q9vjh7	drosophila
296	35	56.5	478	2	Q8ZGA7_YERPE	Q8zga7	yersinia pe
297	35	56.5	480	2	Q40NL8_DESAC	Q40nl8	desulfuromo
298	35	56.5	481	2	Q66CI1_YERPS	Q66ci1	yersinia ps
299	35	56.5	492	2	Q40PS2_DESAC	Q40ps2	desulfuromo
300	35	56.5	500	2	Q4V7B5_RAT	Q4v7b5	rattus norv
301	35	56.5	501	2	Q4KG83_PSEF5	Q4kg83	pseudomonas
302	35	56.5	505	1	TUB_MOUSE	P50586	mus musculu
303	35	56.5	505	1	TUB_RAT	O88808	rattus norv
304	35	56.5	505	2	Q4VA41_MOUSE	Q4va41	mus musculu
305	35	56.5	505	2	Q4SFD0_TETNG	Q4sfd0	tetraodon n
306	35	56.5	506	1	TUB_HUMAN	P50607	homo sapien
307	35	56.5	511	2	Q88KF9_PSEPK	Q88kf9	pseudomonas
308	35	56.5	523	2	Q394G0_BURS3	Q394g0	burkholderi
309	35	56.5	531	2	Q7NSW5_CHRVO	Q7nsw5	chromobacte
310	35	56.5	532	2	Q3A7W0_PELCD	Q3a7w0	pelobacter
311	35	56.5	537	2	Q3MAD0_ANAVT	Q3mad0	anabaena va
312	35	56.5	537	2	Q8YLV7_ANASP	Q8ylv7	anabaena sp
313	35	56.5	545	2	Q63NT3_BURPS	Q63nt3	burkholderi
314	35	56.5	550	2	Q73YZ0_MYCPA	Q73yz0	mycobacteri
315	35	56.5	552	2	Q8DJF1_SYNEL	Q8djf1	synechococc
316	35	56.5	556	2	Q3H600_9ACTO	Q3h600	nocardioid
317	35	56.5	561	2	Q6B007_HUMAN	Q6b007	homo sapien
318	35	56.5	561	2	Q3AHL3_SYNSC	Q3ahl3	synechococc
319	35	56.5	576	2	Q39WT9_GEOMG	Q39wt9	geobacter m
320	35	56.5	582	2	Q3JHQ1_BURP1	Q3jhq1	burkholderi
321	35	56.5	584	2	Q9RTR4_DEIRA	Q9rtr4	deinococcus
322	35	56.5	587	2	Q2T382_BURTH	Q2t382	burkholderi
323	35	56.5	592	2	Q9ZN80_STRCO	Q9zn80	streptomyce
324	35	56.5	602	2	Q3W8V7_9ACTO	Q3w8v7	frankia sp.
325	35	56.5	607	2	Q9L8D4_POLCB	Q9l8d4	polyangium
326	35	56.5	617	2	Q9LWU9_ORYSA	Q9lwu9	oryza sativ
327	35	56.5	620	2	Q3APU9_CHLCH	Q3apu9	chlorobium
328	35	56.5	640	2	Q2R051_ORYSA	Q2r051	oryza sativ
329	35	56.5	654	2	Q2J043_RHOPA	Q2j043	rhodopseudo
330	35	56.5	658	2	Q63XC6_BURPS	Q63xc6	burkholderi
331	35	56.5	718	2	Q37AC3_RHOPA	Q37ac3	rhodopseudo
332	35	56.5	751	2	Q3AN87_SYNSC	Q3an87	synechococc
333	35	56.5	815	2	Q4KS46_9VIRU	Q4ks46	orange-spot
334	35	56.5	881	2	Q4PIH9_USTMA	Q4pih9	ustilago ma
335	35	56.5	922	2	Q4WXJ9_ASPFU	Q4wxj9	aspergillus
336	35	56.5	936	2	Q9DWD4_RCMVM	Q9dwd4	rat cytomeg
337	35	56.5	941	2	Q8QUJ6_9VIRU	Q8quj6	infectious
338	35	56.5	1013	2	Q5CYS5_CRYPV	Q5cys5	cryptospori
339	35	56.5	1017	2	Q2Z4J5_9GAMM	Q2z4j5	shewanella
340	35	56.5	1017	2	Q35VB4_9GAMM	Q35vb4	shewanella
341	35	56.5	1017	2	Q36DD3_9GAMM	Q36dd3	shewanella
342	35	56.5	1020	2	Q3Q7R1_9GAMM	Q3q7r1	shewanella
343	35	56.5	1025	2	Q8EHJ1_SHEON	Q8ehj1	shewanella
344	35	56.5	1039	2	Q31PC4_SYNP7	Q31pc4	synechococc
345	35	56.5	1039	2	Q5N4U6_SYNP6	Q5n4u6	synechococc
346	35	56.5	1041	2	Q33RF7_9GAMM	Q33rf7	shewanella
347	35	56.5	1203	2	Q9A2L9_CAUCR	Q9a2l9	caulobacter
348	35	56.5	1220	2	Q4QAT3_LEIMA	Q4qat3	leishmania